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241 ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWDGTMGCAQBAG-----QDVRGLPGMRT 294
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Sequence 28, Appl
Sequence 28, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 43, Appl
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Sequence 31114, A
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38, Appl
25, Appl
25, Appl
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26, Appli
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37, Appli
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(GGDZ 6/ptodata/1/iaa/PCTUS_COMB.pep:*
(GGDZ 6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-09-912-935-31

US-09-912-935-28

US-09-912-935-34

US-09-912-935-34

US-09-912-935-35

US-09-912-935-35

US-09-12-935-35

US-09-12-935-23

US-09-12-935-23

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US-09-912-935-23

US-09-913-935-23

US-09-459-065-2

US-09-913-065-2

US-09-913-069-28

US-09-913-039-367

US-08-31-080-28

US-08-31-080-28

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         GenCore version (c) 1993 - 2005
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Maximum Match 100%
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLECTIDES
FILE REPERBYCE: 32066/37483
CURRENT PAPLICATION NUMBER: US/09/912,935
CURRENT PAPLICATION NUMBER: PCT/US00/35260
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 36
                      Sequence 4, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 11349, A
Sequence 11373, A
Sequence 2, Appli
Sequence 250, Appli
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Pred. No. 1.7e-168;
0; Mismatches 7; Indels 1.
US-09-041-236-4
US-09-771-467C-4
US-08-836-325-16
US-09-457-571-16
US-09-252-991A-31349
US-09-816-248-17
US-09-816-248-17
US-09-816-248-1373
US-08-820-980-2
US-08-820-980-2
US-08-820-980-2
US-09-248-756A-14379
US-09-248-756A-14379
US-09-461-325-550
US-09-248-756A-14379
US-09-461-325-550
US-09-1012-542-550
US-10-012-542-550
US-10-115-123-550
US-10-115-123-550
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; Sequence 36, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
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94.2%;
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; ORGANISM: Homo sapiens
US-09-912-935-36
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APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: MOTHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: MOTHODS AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/33483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 40
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                                                                                                                                                        DB 4; Length 529;
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Best Local Similarity 56.5%; Pred. No. 1.9e-96;
Matches 205; Conservative 63; Mismatches 88
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Patent No. 6673904
GENERAL INFORMATION:
; SEQ ID NO 28
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-28
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ORGANISM: Homo
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                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REPERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN Version 3.0

SEQ ID NO 31
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Sequence 28, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
MITCHOOLE INVENTION:
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                                                                                                                                                        Sequence 31, Application US/09912935 Patent No. 6673904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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US-09-912-935-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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LGTI 358
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                                                                                                           RESULT 2
US-09-912-935-31
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Best Local S
Matches 205
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Patent No. 6673904

GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912, 935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
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Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION UNBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SFDFPFYGHFLREITVATGGFIYTGEVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFDN 119
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47.2%; Score 1047.5; DB 4; Length Best Local Similarity 56.9%; Pred. No. 1e-94;
Matches 203; Conservative 55; Mismatches 88; Indels
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Best Local Similarity 51.3%; Pred. No. 3.2e-94;
Matches 203; Conservative 67; Mismatches 112;
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SEQ ID NO 38
LENGTH: 530
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version
                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-912-935-35
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US-09-912-935-38
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US-09-912-935-38
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 32066/37483
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 34
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GPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKEKMCENTEPVETSSRTTT 394
                                                                                                                                                                                                                            T--SPSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ-NNLSPKTKGTPVHL 407
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                                                               PVKTGLSDAFM1LNPSPDVPESRRRS1FEYHR1ELDPSKVTSMSAVEFTPLPTCLOHRSC
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57.2%; Pred. No. 2e-95;
ive 59; Mismatches 86; Indels
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; Patent No. 6673904
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US-09-912-935-35
; Sequence 35, Application US/09912935
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ORGANISM: Homo sapiens
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us-uy-loa-342A-25

j Sequence 25 Application US/09764325A

patent No. 6667391

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Tang, Y. T.

APPLICANT: Tang, Y. T.

APPLICANT: Childs, John

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides

TITLE OF INVENTION WHORER: US/09/764,325A

CURRENT APPLICATION NUMBER: 09/547,358

PRIOR PELING DATE: 2000-04-07

PRIOR PELING DATE: 2000-04-07

PRIOR PLING DATE: 2000-04-07

PRIOR PLING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 25

LENGTH: 332
                                                                                                                                                          CENTEPVETSSRITITIGATITY CFRVLTTRRAVISQFPISLPTEDDIKIALHLKDNGAS 302
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                                                                                                                          CEDEQDEDHDSASPDT--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ 393
                                                  183 VEMTPLPTCLQFNRCGFCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKERM
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42.7%; Score 948; DB 4; Length 392;
Best Local Similarity 57.9%; Pred. No. 6e-85;
Matches 184; Conservative 51; Mismatches 77; Indels
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US-09-764-325A-25
                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-764-325A-25
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| GENERAL INFORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Tang, Y. T. |
| APPLICANT: Tang, Y. T. |
| APPLICANT: Chao, Cheng-Chi |
| APPLICANT: Chao, Cheng-Chi |
| APPLICANT: Chao, Cheng-Chi |
| APPLICANT: Childs, Jone |
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell |
| TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides |
| TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides |
| TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides |
| TITLE OF INVENTION WIMBER: 09/647,358 |
| FILE REFERENCE: 30266/37630A |
| CURRENT APPLICATION NUMBER: 09/545,714 |
| PRIOR APPLICATION NUMBER: 09/545,714 |
| PRIOR APPLICATION NUMBER: 09/488,725 |
| PRIOR PELLING DATE: 2000-04-07 |
| PRIOR PELLING DATE: 2000-01-21 |
| NUMBER OF SEQ ID NOS: 25 |
| SEQ ID NOS: 26 |
| TENTING DATE: 2000-04-07 |
| SEQ ID NOS: 26 |
| SE
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-hes 77; Indels
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Matches 184; Conservative
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ORGANISM: Homo sapiens
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158

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KEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSA 278
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                                                                                                                                                                                                                                                                                                                                          183 VEMTPLPTCLOFNRCGPCVSSQIGFNCSWCSKLORCSSGFDRHRQDWVDSGCPEESKEKM
                                                                                                                                159 APLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAY
                                          99 RSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYV
  6; Gaps
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APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING BATE: October 26, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09181706
| Patent No. 6130068
| GENERAL INFORMATION:
| APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
| APPLICANT: Melanie K. Spriggs, Michael R. Johnson
| TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
| TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESSE: ADDRESSEE: Janis C. Henry
| STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: October 28, 1998
CLASSIFFCATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
51; Mismatches
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REGISTATION NUMBER: 26:
REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
Matches 184; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                             GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT FILING DATE: 2010-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 392
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 APLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAY 218
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57.9%; Pred. No. 6e-85;
tive 51; Mismatches 77; Indels
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                                Sequence 23, Application US/09912935
Patent No. 6673904
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SEQ ID NO 25
LENGTH: 392
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-23
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ORGANISM: Homo sapiens
US-09-912-935-25
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Best Local Similarity
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                -09-912-935-23
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US-09-912-935-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 LLLSSSLVEALDVWAGVFSAAAGEGOERRSPTTTALCLFRMSEIOARAKRVSWDFXTAES 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 HCKEGDOPERVOPIASSTL-----IHSDLTSV-YGTVVM-----NRTVLF 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ
                                                                                                                                                                                                                                                                                         22 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
                                                                                                                                                                                                                                                                                                                                                                               78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF----
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                                                                                                                                                                                                      DB 3; Length 1568;
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Patent No. 6187909
GENERAL INFORMATION:
GENERAL INFORMATION:
SPATIGAM:
SPATIGAN:
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Janis C. Henry
                                                                                                                                                                                                    5.2%; Score 115.5; DB 3; 20.6%; Pred. No. 0.074; tive 42; Mismatches 118;
                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
RAMS: Henry, Janis C
REGISTRATION NUMBER: 34,347
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 amino acids
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51 University St.
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                                                                                                                                                                                                                         Best Local Similarity 20.69
Matches 77; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CITY: Seattle
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COUNTRY: US
ZIP: 98101
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                                                                                                                                                        US-09-458-791-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------BQQLLKVILGENLTSNCPEVIYEIKEE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 TPV-----FYKLVPDP-----VKNIYIY------LTAGKEVRRIRVANCHKKS 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 344
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                                                                                                                                                                                                                                                                                                                                                                                                                             353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVVM-----NRTVLF 391
                                                                                                                                                                                                      22 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS 77
                                                                                                                                                                                                                                                  256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR------R
                                                                                                                                                               Gaps
                                                                                                                                                             42; Mismatches 118; Indels 137;
                                                                                                                   Length 1568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09458791
Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                              DB 3;
                                                                                                              Query Match 5.2%; Score 115.5; DB Best Local Similarity 20.6%; Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
FILING DATE: 10-Dec-1999
CLASSIFICATION: <u >Unknown></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
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516 KEKTTVTMVGSFSP 529
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COMPUTER READABLE FORM:
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                                                                                                                                                          77; Conservative
                                         MOLECULE TYPE: protein US-09-181-706-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SD
      amino acid
                              linear
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US-09-458-791-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 LILSSSLVEALDVWAGVFSAAAGEGQERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----DEPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVVM-----NRTVLF 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 1568;
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APPLICANT: SPRIGGS, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2%; Score 115.5; DB 3; 20.6%; Pred. No. 0.074; iive 42; Mismatches 118;
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SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/958,598
FILING DATE:
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
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Patent No. 6562949
                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189
                                                                                                                      TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
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STREET: 51 University St.
CITY: Seattle
                                                                                   (206) 470-4189
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 20.6°
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. F
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                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                US-09-459-066-2
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256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR------R 292
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; Pred. No. 0.074;
42; Mismatches 118;
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                                      34,347
                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1568 amino acids
                                                                                                                                                                                                                                                                                                        n 5.2%;
Similarity 20.6%;
                                                                                                TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
ATTORNEY/AGENT INFORMATION:
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                   NAME: Henry, Janis C
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 20.6%
Matches 77; Conservative
                                                                                                                                                                                            ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-459-065-2
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(c) 1993 - 2005 Compugen Ltd.
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No.
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Sequence 36, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 36
SEQ ID NO 36
LENGTH: 431
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US-09-912-935-38
US-09-912-935-38
US-09-912-935-38
US-09-912-935-38
Sequence 38, Application US/09912935
Facent No. 6673904
GENERAL INFORMATION:
APPLICAMT:
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERRENCE: 32066/37483
CURRENT FILING DATE: 2001-07-24
FRIOR APPLICATION NUMBER: PCT/US00/35260
FRIOR PILING DATE: 2000-12-23
SOFTWARE: PAGENT IN VEXION 3.0
SEQ ID NO 38
                        Sequence 17, Appl
Sequence 17, Appl
Sequence 130, Appl
Sequence 131, Appl
Sequence 15, Appl
Sequence 191, Appl
Sequence 191, Appl
Sequence 191, Appl
Sequence 191, Appl
Sequence 1717, Appl
Sequence 17517, Appl
Sequence 17517, Appl
Sequence 17517, Appl
Sequence 17517, Appl
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        Sequence
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US-09-358-055B-132
US-09-245-041-17
US-09-838-055B-17
US-09-938-055B-131
US-09-35B-055B-131
US-09-35B-055B-131
US-09-38-055B-131
US-09-98-055B-15
US-09-98-055B-15
US-09-98-05-15
US-09-270-76-238-15
US-09-270-76-236-3
US-09-270-76-236-3
US-09-370-83B-191
US-09-83B-191
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ORGANISM: Homo sapiens
US-09-912-935-36
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      QEW 271
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Gaps

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**Section 10. Section 10. Sect
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Patent No. 6673904
; GENERAL INPORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
ATITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE;
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth Factor-Like Polypeptides and Polynucleotides
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Pred. No. 1.1e-24;
9; Mismatches 12; Indels
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Pred. No. 1.1e-24;
9; Mismatches 12; Indels
                        FILE REFERENCE: 30266/37630A
CURRENT APPLICATION NUMBER: US/09/764,325A
CURRENT FILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: 09/547,358
FRIOR PILING DATE: 2000-04-11
FRIOR FILING DATE: 2000-04-07
FRIOR APPLICATION NUMBER: 09/545,714
FRIOR APPLICATION NUMBER: 09/548,725
FRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 25
LENGTH: 392
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Best Local Similarity 67.7%;
Matches 44; Conservative S
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Best Local Similarity 67.7%;
Matches 44; Conservative
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ORGANISM: Homo sapiens
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227 ODWVD 231
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APPLICANT: Labat, Ivan
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Aze, Nancy K.
APPLICANT: Chao, Cheng-Chi
APPLICANT: Childs, John
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
FILE REFERENCE: 30266/37630A
FILE REPERENCE: 2001-01-16
FRIOR APPLICATION NUMBER: 09/547,358
FRIOR FILING DATE: 2000-04-11
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Sequence 25, Application US/09764325A

Patent No. 6667391

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Chao,                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                      Length 530;
                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                      Score 264; DB 4;
Pred. No. 1.2e-24;
9; Mismatches 12;
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Best Local Similarity 67.7
Matches 44; Conservative
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ORGANISM: Homo sapiens
US-09-764-325A-23
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364 QDWVD 368
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227 QDWVD 231
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                                  ; TYPE: PRT
; ORGANISM: Mouse
US-09-912-935-38
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US-09-764-325A-23
    LENGTH: 530
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Gaps

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Sequence 31, Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PRING PAPLICATION NUMBER: PCT/US00/35260
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
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Pred. No. 1.3e-24;
9; Mismatches 12.
                 SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 449
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Best Local Similarity 67.7%;
Matches 44; Conservative
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Matches 44; Conservative
NUMBER OF SEQ ID NOS: 53
                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-34
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364 QDWVD 368
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SEQ ID NO 28
LENGTH: 529
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: 'US/09/912,935
CURRENT PILLING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 35
LENGTH: 425
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Sequence 34, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
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                                                                                                                                                                                                                                                                  71.1%; Score 263; DB 4; Length 392; 67.7%; Pred. No. 1.1e-24; ive 9; Mismatches 12; Indels
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Pred. No. 1.3e-24;
9; Mismatches 12; Indels
             CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
LENGTH: 392
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Best Local Similarity 67.7%;
Matches 44; Conservative
FILE REFERENCE: 32066/37483
                                                                                                                                                                                                                                                                                                             44; Conservative
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-09-912-935-35
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262 QDWVD 266
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227 QDWVD 231
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US-09-912-935-35
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                                                                                                                                                                                                                                                                      Query Match
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1 YHRIELDPSK-----VTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSG 55
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                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.3%; Score 101; DB 3; Length 1568; Best Local Similarity 29.7%; Pred. No. 0.00079; Matches 22; Conservative 15; Mismatches 27; Indels 10
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Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION:
RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIO
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
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APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: <unknown>
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APPLICATION WUNBER: 08/958,598
FILING DATE: 28-007-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,347
REFRENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206/470-4189
TELEFAX: (206)233-0644
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
                        October 28, 1998
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,3
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COMPUTER READABLE FORM:
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MOLECULE TYPE: protein

US-09-181-706-2
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  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                           CLASSIFICATION:
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FILE REPERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-107-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOPTWARE: Patentin version 3.0
SEQ ID NO 40
LENGTH: 529
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                                                                                                                                                                                         304 YHRVELQMSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHR 363
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                                                                                                                   Gaps
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                                                                   Query Match 71.1%; Score 263; DB 4; Length 529; Best Local Similarity 67.7%; Pred. No. 1.6e-24; Matches 44; Conservative 9; Mismatches 12; Indels
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| Patent No. 6130068
| GENERAL INFORMATION:
| APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
| APPLICANT: Robert F. DuBose Richard S. Johnson
| TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
| TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS: ADDRESS: JANIS C. Henry
| STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/09912935
Patent No. 6673904
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ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-912-935-28
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Matches 44; Conserv
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364 QDWVD 368
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364 QDWVD 368
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US-09-459-065-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.3%; Score 101; DB 3; Length 1568; Best Local Similarity 29.7%; Pred. No. 0.00079; Matches 22; Conservative 15; Mismatches 27; Indels 10
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APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDR
                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
TELECOMMUNICATION INFORMATION TELEPHONE: (206)470-4189
                                                                                                                                                                                                         LENGTH: 1569 amino acids TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
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Patent No. 6187909
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ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REPRENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                                          TELEFAX: (206)233-0644
                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 GDCVHSENLENWLD 498
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Best Local Similarity 29.7%
Matches 22, Conservative
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LENGTH: 1568 amino acids
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426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCTFQ 484
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                                                                                                                                                                                                                                       Sequence 2, Application US/09459065
; Sequence 2, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 31 University St.
; CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 28, 2005, 22:14:14 Job time : 6.53163 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                             485 GDCVHSENLENWLD 498
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TELEPHONE: (ZUD)...
TELEPHONE: (ZUD)...
TO NO:
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INFORMATION FOR ENQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
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Compugen Ltd.
GenCore version (c) 1993 - 2005
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(without alignments) 1129.372 Million cell updates/sec	
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1 ALSPQPGAGHDEGPGSGWAA......GLQNNLSPKTKGTPVHLGTI 410 US-09-918-715-230_COPY_18_427 2218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq_23Sep04:*
1: geneseqp1900s:*
2: geneseqp2000s:*
3: geneseqp2000s:*
5: geneseqp2001s:*
5: geneseqp2013s:*
6: geneseqp2013s:*
7: geneseqp2033s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Abb90749	Abu54456	Adi21063	Adh13230	Adi21554	Adi21553	Abb90723	Abu54430	Adi21064	Aab43131	Abb90783	Abb90729	Abu54436	Abu54490	Aab85400	Abo01434	Adb65558	Aam39067	Aab85396	Abo01430	Aab31211	Aab85394	Aau29259	Aam39068	Abb90734
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ALIGNMENTS

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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                         Human Tumour Endothelial Marker polypeptide SEQ ID NO 230,
                                                                                                                                                                                                                                                                             St Croix B, Kinzler KW, Vogelstein B;
ABB90749 standard; protein; 500 AA.
                                                                                                                                                                                                                 02-AUG-2000; 2000US-0225599P.
11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
                                                                                                                                                                                                01-AUG-2001; 2001WO-US024031.
                                                                                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS.
                                      (first entry)
                                                                                                                                                          WO200210217-A2.
                                                                                                                                        Homo sapiens
                                      30-MAY-2002
                                                                                                                                                                              07-FEB-2002.
                                                                                                                      psoriasis.
                  ABB90749;
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WPI; 2002-291856/33. N-PSDB; ABL92103.

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.

Claim 1; Page 206-207; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB907569. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic

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retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL921996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
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100.0%; Pred. No. 2.7e-211;
ive 0; Mismatches 0;
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2002US-0354262P.
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410; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317
                                                                                                                                                                               The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polynucleotide sequences encoding them are useful for detecting, polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiodenesis, for for identifying candidate drugs for treating tumours. The present for identifying candidate drugs for treating tumours. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as tumor endothelial
                                                             New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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Pred. No. 2.7e-211;
0; Mismatches 0;
                                                                                                                                                      Disclosure; Page 221-222; 374pp; English.
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            WPI; 2003-093016/08.
N-PSDB; ABX72028.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 500 AA;
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                                                                                                                    psoriasis
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This invention relates to a novel method for the prediction, diagnosis, or prognosis of malignant neoplasia by the detection of at least two markers. The invention may also be useful for the development of cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia such as breast cancer, ovarian cancer, pastric cancer, colon cancer, oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell ung cancer. The polynucleotides and polypeptides defined in the specification, antisense polynucleotides targetting the polynucleotides, antibodies targetting either one of the polynucleotides or polypeptides, and compounds identified by the screening methods are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Predicting, diagnosing or prognosing malignant neoplasia by detecting at least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                           malignant neoplasia; cytostatic; breast cancer; ovarian cancer; gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer; bladder cancer; non-small cell lung cancer; human.
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                                                                                                        GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLONNLSPKTKGTPVHLGTI
                                                                            GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
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llarity 100.0%; Pred. No. 2.7e-211;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                Human malignant neoplasia-related protein SeqID79,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 79; 267pp; English.
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                                                                                                                                                                                                                                                    ADH13230 standard; protein; 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAY-2003; 2003EP-00010447.
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13-FEB-2003; 2003EP-00003112.
                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-073279/08
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Best Local Similarity
Matches 410; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1365034-A2
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                                                                            361
                              318
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                                                                                                                                                                                                   RESULT 4
ADH13230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptide are useful in diagnostics, forenaise, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incissions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAFWILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 77
       tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                         Wang J;
Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
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Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                         , Goodrich RW, Ren F, Zhang
Wehrman T, Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 314; 156pp; English.
                                                                                                                                                                                                   19-SEP-2002; 2002WO-US029964.
                                                                                                                                                                                                                                                 19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739.
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Best Local Similarity 100.
Matches 410; Conservative
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N-PSDB; ADI21779.
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                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Asundi V,
Ghosh M, Xue AJ,
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 500 AA;
                                                                                                   WO2003025148-A2
                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replacement.
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19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739.
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Best Local Similarity 100.
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                                                                                                                                                                                          polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; and cell disorder; lymphoid cell disorder; lissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
                    PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
                                                                          SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                              DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                      DAFMILNDSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 317
                                                                                                                                                                                                                                                                                                          LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 360
                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements.
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Vang D;
PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL
                                                                                                                                                      GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
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Drmanac RT,
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g G, Zhou P,
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Wehrman T,
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13-SEP-2002; 2002US-00323739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Asundi V,
Ghosh M, Xue AJ, V
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-354603/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADI21334.
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The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 2218; DB 7;
; Pred. No. 3e-211;
0; Mismatches 0;
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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; attiangyogenic; tumour; necemplesses; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                           Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.
                                                                                                                                                                                                                                                                                                                                                                                              St Croix B, Kinzler KW, Vogelstein
                                                                                                                                                                                                                                                                                                                 11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                             (first entry)
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                                                                                                                                                                                                            WO200210217-A2.
                                                                                                                                                                                Homo sapiens.
                             30-MAY-2002
                                                                                                                                                                                                                                          07-FEB-2002
                                                                                                                                                  psoriasis.
 ABB90723;
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                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or cregeneration, in wound healing, in tissue repair and replacement, in healing of burns, inclusions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                 New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
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                                             Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
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                                                           Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
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                                            Zhang J, Zhao QA,
ou P, Drmanac RT,
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                                            Goodrich RW, Ren F, Zhang
thrman T, Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2218; DB 7
100.0%; Pred. No. 3e-211;
iive 0; Mismatches 0
                                                                                                                                                                                                                          Example 3; SEQ ID NO 804; 156pp; English.
                                                          Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 410; Conservative
                                                                                                    WPI; 2003-354603/33.
N-PSDB; ADI21333.
                                            Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                        Tang YT, Asundi V
Ghosh M, Xue AJ,
Haley-Vicente D;
               HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 527 AA;
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90149, abb90750 and ABB90765. The antibodies which bind to TEM proteins have cyrostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and tr TEM genes and the encoded proteins (ABE92075-ABE92141 and ABB90781-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABE92042-ABE92041 and ABE92143-ABE92191; normal endothelial markers (NEM) ABE92042-ABE92044; and pan-endothelial markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2218; DB 5; Length 1002; 100.0%; Pred. No. 8e-211; ive 0; Mismatches 0; Indels 0;
Disclosure; Page 125-128; 331pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 410; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1002 AA;
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ABB90723 standard; protein; 1002 AA.

RESULT 7 ABB90723 ID ABB9

240

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New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                       myeloid cell disorder; lymphoid cell disorder;
bone cartilage tissue growth; tendon tissue growth;
ligament tissue growth; nerve tissue growth; regeneration; wound healing;
tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
                                                           PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                          SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
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                                                                                                                                                                                                                                                                                                     LTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 360
                                                                                                                                      SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
                                                                                                                                                                                                                                                               DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD
                  GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
                                                                                                                                                                                                 ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                                                                                                                                                                                                                                                                                                                                              GDLTTTSSSIFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      forensic; nutritional source; damaged tissue; diseased tissue;
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ou P, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-2002; 2002WO-US029964.
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13-SEP-2002; 2002US-00323739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghosh M, Xue AJ,
Haley-Vicente D;
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LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDISFSPYD 360
                                                                      820 LTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polynthelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynthelectide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting necangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drogs for treating tumours. The present for identifying candidate drogs for treating tumours. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified human transmembrane protein, designated as tumor endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marker (TEM) 3, useful for detecting, diagnosting or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
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                                                                                                                                                                                                                                                                                                                               Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; neoangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
                                                                                                      GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 122-124; 374pp; English.
                                                                                                                                                                                                                                                                                                     endothelial marker TEM 8.
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                                                                                                                                                                                                               ABU54430 standard; protein; 1002
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2002US-0354262P.
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06-FEB-2002;
                                                                                                                                                                                                                                                                                                        Human tumour
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                 260
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The invention relates to an isolated polynucleotide encoding

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polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or respensation, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRARESPGHVSEPDRTQLSQDLGGGTLLAMDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 2134; DB 7; Length 488;
Pred. No. 6e-203;
0; Mismatches 0; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                           96.2%;
97.1%;
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nes 398; Conservative
                                                                                                                                                                                                                                                                                                                                                                  Sequence 488 AA;
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Best Local S
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AAC74446 to AAC77606 encode the proteins given in ABB40237 to AAB843397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
cequences have activities such as: cytostatic; hepatotropic; valnerary;
antipsoriatic; antiparkinsonian; mootropic; neuroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; immunosuppressive; antidiabetic; hypotensive;
dermatological; antirheumatic; antidiabetic; hypotensive;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; antirheumatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
cc, or preventing or treating pathological conditions associated with an
CORFX-associated disorder. The nucleic acids can be used to express ORFX
proteins in gene therapy vectors. The proteins and nucleic acids may be
used to treat cancers, proliferative disorders, neurodegenerative
disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
cdisorders mellitus, hypertension, hypothyroidism, cholesterol ester
storage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
enhance coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SFDFFFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
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bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 4955; 5507pp; English
                                                                                                                                                                                                                                            31-MAR-1999; 99US-0127607P.

02-APR-1999; 99US-0127636P.

05-APR-1999; 99US-0127728P.

30-MAR-2000; 2000US-00540769.
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                                                                                                                                                                                                                                                                                                                                                                                                        Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
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                                                                                                               WO200058473-A2.
                                                                     Homo sapiens.
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neconglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
                                                                                                                                                     SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                  139 SFDFPFYGHPLRQITIATGGFIFMGDMLHRMLTATQYVAPLMANFNPGYSDNSTVAYFDN 198
                                                                                                                                                                                                    DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTFLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                                       301 LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 360
 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antianglogenic; tumour; neoanglogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis.
                                                                                                                                     GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                        GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI 410
                                                                                                                                                                                                                                                                                                                                                            Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                                                                                     Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangogenesis; vascularised tumour; neoappolycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
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                                                                        LIFINCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDT 399
                                                    LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDT 354
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                                                                                                                                                                                                                                                                       Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.
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11-AUG-2000; 2000US-0224360P.
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Matches 331; Conservative
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N-PSDB; ABL92136.
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genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
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                                                                                               Gaps
     are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191, endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; neoangiogenesis; antimne response; cytostatic; antidabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                                           81.1%; Score 1799.5; DB 5
80.7%; Pred. No. 1.2e-169;
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2002US-0354262P.
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                                                                                              331; Conservative
                                                                           Query Match
Best Local Similarity
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06-FEB-2002;
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                                                                                endothelial
                                                                                                                                                                                                                                                          The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psorlasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a mouse TEM protein
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                                                      New purified human transmembrane protein, designated as tumor endothel marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 PDNRTRVVEDNHNYYVSRVYGPGEKQSQDLWVDLAVANRSHVKIHRILSSSHRQASRVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 GTVEVVQWDHVYLQDREDRGSFTFQAALHRDGRIVFGYKEIPMAVLDISSAQHPVKAGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAFMILNSSPEVPESQRRTIFEYHRVELDSSKITTTSAVEFTPLPTCLQHQSCDTCVSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 1799.5; DB 6; 80.7%; Pred. No. 1.2e-169; ive 39; Mismatches 39;
                                                                                                                                                                                                                  Disclosure; Page 147-148; 374pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 80.7
Matches 331; Conservative
2003-093016/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 500 AA;
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ABU54490
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175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFDFPFYGHPLRQITIATGGFIFMGDMLHRMLTATQYVAPLMANFNPGYSDNSTVAYFDN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                                                                            New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal marker (DEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a mouse TEM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIFNCSWCHVLORCSSGFDRYROEWLIYGCAQEABGKTCEDFQDDSHYSASPDSSFSPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDISFSPYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                       Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.1%; Score 1799.5; DB 6; 80.7%; Pred. No. 1.2e-169; ive 39; Mismatches 39;
                                                                                                                                                                                                                                       Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 339-340; 374pp; English.
                                                                                                                                                                                                                                       St Croix B,
                                                                                                                          10-APR-2002; 2002WO-US008253
                                                                                                                                                        11-APR-2001; 2001US-0282850P.
06-FEB-2002; 2002US-0354262P.
                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80., Matches 331; Conservative
                                                                                                                                                                                                                                                                     WPI; 2003-093016/08.
N-PSDB; ABX72061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                     Carson-Walter E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 500 AA;
                                                             WO200283874-A2
                                                                                            24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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Best Local S
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The invention provides novel human stem cell growth factor-like polypeptides and polymcleotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polymcleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may aid spatients in need of transplants. They can also be used as nutritional supplements. The present sequence represents a tumour endothalial marker of precursor protein, homologous to a stem cell growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHP 180
                                                                                                                                                                                                                                                                 Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; hutritional supplement; cytostatic; nootropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; tumour endothelial marker 7 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IAMDTLEDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Childs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.9%; Score 1795; DB 4; Length 431; llarity 94.2%; Pred. No. 2.8e-169; Conservative 0; Mismatches 7; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mize NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee J,
                                                                                                                                                                                                     Tumour endothelial marker 7 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 149-150; 154pp; English.
Ā
AAB85400 standard; protein; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
7-APR-2000; 2000US-00545714.
11-APR-2000; 2000US-00547358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-2000; 2000WO-US035260.
                                                                                                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-451909/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153500-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Simi
Matches 343;
                                                                                                                                      17-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001
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174

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        Qy
        235 VKTGLSDAFMILAPSPDVPESRRRSIFETHRIELDPSKVTSMSAVEFTPLFTCLQHRSCD 294

        Db
        181 VKTGLSDAFMILAPSPDVPESRRRSIFETHRIELDPSKVTSMSAVEFTPLFTCLQHRSCD 240

        Qy
        295 ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEW DDYGCAQABAGRMCEDPQD------BD 346

        Db
        241 ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEW DDTYGCAQABAGRMCEDPQD------BD 346

        Qy
        347 HDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVH 406

        Db
        295 TTSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVH 354

        Qy
        407 LGTI 410

        Db
        355 LGTI 358

        Search completed: January 28, 2005, 22:05:04

        Job time: 132.231 secs
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January 28, 2005, 21:59:20 ; Search time 112.059 Seconds (without alignments) 1321.880 Million cell updates/sec
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2218
1. ALSPQPGAGHDEGPGSGWAA........GLONNLSPKTKGTPVHLGTI 410
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/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:
/cgn2_6/ptodata/1/pubpaa/US10_NEW-PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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19:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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;	230, App	Appl	Apr	i Iddi	179, App	Apr	ppli	Appli	Apr	Apr	6, Appli	Apr	Apr
_	230,	79,	230,	2, Appl	179,	179,	4, A	5, A	192,	297,	6, A	192,	297,
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	230	79	230	7	179	179	4	-5	192	297	9-	192	297
	US-09-918-715-230	-10-435-696-	-10-474-794-	-10-357-819-	-09-918-715-	-10-474-794-	-10-357-819-	-10-156-487A	-09-918-715-	-09-918-715-	-10-156-487A	-10-474-794-	-10-474-794-
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% Query Match Length DB	200	200	200	200	1002	1002	488	502	200	200	200	200	200
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	96.2	94.4	81.1	81.1	81.1	81.1	81.1
Score	2218	2218	2218	2218	2218	2218	2134	2093	1799.5	1799.5	1799.5	1799.5	1799.5
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PDNRTRVVEDNHSYYVSRLYGPSEPHSRELMVDVAEANRSQVKIHTILSNTHRQASRVVL 120

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36, 336, 331, 331, 1189, 1200, 4472, 4472, 4472, 4472,	Sequence 472, App Sequence 472, App
0 US-09-912-935-36 4 US-10-168-365-36 4 US-10-104-047-3712 0 US-09-918-35-31 0 US-09-918-715-189 0 US-09-918-715-200 0 US-09-912-935-28 0 US-09-912-935-28 0 US-09-912-935-40 1 US-10-105-586-472 3 US-10-065-586-472 4 US-10-174-590-472 4 US-10-174-590-472 4 US-10-174-591-472	4 US-10-1/6-485-472 4 US-10-176-914-472 4 US-10-176-914-472 4 US-10-176-915-472 4 US-10-173-706-472 4 US-10-175-738-472 4 US-10-175-738-472 4 US-10-176-787-472 4 US-10-176-787-472 4 US-10-186-552-472 4 US-10-180-552-472 4 US-10-174-588-472 4 US-10-174-588-472 4 US-10-174-588-472
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ALIGNMENTS

(BSULT 1 15-09-918-715-230		
Sequence 230, Application US/09918715		
Publication No. US20030017157A1		
GENERAL INFORMATION:		
щ		
APPLICANT: Bert Vogelstein		
APPLICANT: Kenneth Kinzler		
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS		
FILE REFERENCE: 1107.00134		
CORRENT APPLICATION NUMBER: 05/09/918,/15		
CURRENT FILLING DATE: ZUOI-U8-01		
PRIOR APPLICATION NUMBER: 60/222,539		
FRIOR FILLING DATE: ACCOUNTS OF THE PROPERTY O		
PRIOR FILING DATE: 2000-08-11		
PRIOR APPLICATION NUMBER: 60/282,850		
PRIOR FILING DATE: 2000-04-11		
NUMBER OF SEQ ID NOS: 358		
SOFTWARE: FastSEQ for Windows Version 3.0		
SEQ ID NO 230		
LENGTH: 500		
TYPE: PRT		
ORGANISM: Homo sapiens		
JS-09-918-715-230		
100.08;		
Best Local Similarity 100.0%; Pred. No. 1.5e-203; Marches 410: Conservative 0: Mismatches 0: Indels 0: Gabs	0	_
1 ALSPOPGAGHDEGPGGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 6	r 60	
DS 18 ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 7	L 77	

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18 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 LIFNCSWCHVIQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 377
318 LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDISFSPYD 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELMVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstain, Bert
APPLICANT: Wigelstain, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR PLING DATE: 2001-04-11
PRIOR PLING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                 ; Sequence 230, Application US/10474794; Publication No. US20040213793A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10357819; Publication No. US20040259774A1; GENERAL INFORMATION:
APPLICANT: Alvarez, Enrique; APPLICANT: Edinger, Shlomit R.
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US-10-357-819-2
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APPLICANT: Murnes, Marc
APPLICANT: Munnes, Marc
APPLICANT: Murnes, Marc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
CURRENT PLING DATE: 2003-05-09
PRIOR PILING DATE: 2003-02-13
PRIOR PILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
SOFTWARE: Patentin version 3.1
SEQ ID NO 79
LENGTH: 500
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                                                                                        SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 197
                                                                                                                                                         GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS 240
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                                                      SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                                                                                                                                                                                                                       DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 317
                                                                                                                                                                                                                                                                                                                                                                                                       LIFNCSWCHVLORCSSGFDRYROEWMDYGCAORAEGRMCEDFODEDHDSASPDISFSPYD 377
     PDNRTRVVEDNHSYYVSRLYGPSEPHSRELMVDVAEANRSQVKIHTILSNTHRQASRVVL 137
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                                                                                                                                                                                     GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPWSVPEISSSQHPVKTGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-435-696-79
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US-10-435-696-79
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301 LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDISFSPYD
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                                                                                                     361 GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bert Vogelstein
APPLICANT: Renneth Kinzler
TITLE OF INVENTION: ENNOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT PILLING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR PILLING DATE: 2000-08-02
PRIOR PILLING DATE: 2000-08-11
PRIOR PILLING DATE: 2000-08-11
PRIOR PILLING DATE: 2000-08-11
PRIOR PILLING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FRAESEQ for Windows Version 3.0
SEQ ID NO 179
LENGTH: 1002
                                                                                                                                                                                                                                                                                          Sequence 179, Application US/09918715
Publication No. US20030017157A1
GRNERAL INFORMATION:
APPLICANT: Brad St. Croix
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US-10-474-794-179
IS-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 410; Conservative
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Ratturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
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CURRENT APPLICATION NUMBER: US/10/357,819

CURRENT PILMG DATE: 2003-02-03

FRIOR PILING DATE: 2000-03-08

FRIOR PLING DATE: 2000-03-08

FRIOR PLING DATE: 2000-05-09

FRIOR PLING DATE: 2000-05-09

FRIOR PLING DATE: 2000-05-14

FRIOR APPLICATION NUMBER: 09/783,436

FRIOR PLING DATE: 2002-02-25

FRIOR APPLICATION NUMBER: 06/353,301

FRIOR APPLICATION NUMBER: 60/355,099

FRIOR APPLICATION NUMBER: 60/355,099

FRIOR PLING DATE: 2002-02-25

FRIOR APPLICATION NUMBER: 60/355,099

FRIOR PLING DATE: 2002-02-20

FRIOR PLING DATE: 2002-02-22

FRIOR PLING DATE: 2002-02-21

FRIOR PLING DATE: 2002-02-22

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Best Local Similarity 100.
Matches 410; Conservative
                                                                                               Ji, Weizhen
Kekuda, Ramesh
                                                                            Guo, Xiaojia
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ORGANISM: Homo sapiens
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US-10-156-487A-5
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APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelaterin, Bert
APPLICANT: Wobelaterin, Bert
APPLICANT: Kincler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERBNCE: 1107.00179
CURRENT APPLICATION NUMBER: 05/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 179
LENGTH: 1002
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                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2218; DB 17;
100.0%; Pred. No. 4.5e-203;
tive 0; Mismatches 0;
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Miller, Charles E.
Padigaru, Muralidhara
Patturajan, Meera
Rastelli, Luca
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Publication No. US20040259774A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alvarez, Enrique APPLICANT: Edinger, Shlomit R APPLICANT: Gangolli, Esha A. APPLICANT: German, Linda APPLICANT: Gorman, Linda APPLICANT: Gorman, Linda APPLICANT: Guo, Xasojia APPLICANT: Kekuda, Ramesh APPLICANT: Kekuda, Ramesh APPLICANT: Padigaru, Muralidh APPLICANT: Padigaru, Meral APPLICANT: Patigaru, Meral APPLICANT: Rastelli, Luca APPLICANT: Rastelli, Luca APPLICANT: Rieger, Daniel K. APPLICANT: Shenoy, Suresh G.
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Best Local Similarity 100.
Matches 410; Conservative
                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-474-794-179
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US-10-357-819-4
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APPLICANT: SINGRES, KINDERLY A.
APPLICANT: STORG, Mei
APPLICANT: SLORG, Mei
APPLICANT: Zhong, Mei
TILB. OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
FILE REPREBACE: 21402-258A
CURRENT APPLICATION NUMBER: US/10/357,819
FRICR FILING DATE: 2000-05-31
FRICR FILING DATE: 2000-05-31
FRICR FILING DATE: 2000-05-31
FRICR FILING DATE: 2000-02-25
FRICR FILING DATE: 2000-02-25
FRICR FILING DATE: 2002-02-25
FRICR FILING DATE: 2002-02-35
FRICR FILING DATE: 2003-03-35
FRICR FILING DATE: 2003-
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Best Local Similarity 97.1%; Pred. No. 1.7e-195;
Matches 398; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-192
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Matches 331;
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Best Local
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            APPLICANT: Juan, Todd
APPLICANT: Dass, Michael B.
APPLICANT: Dass, Michael B.
APPLICANT: Oliner, John
TITLE OF INVENTION: Tunor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT PELLING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/293,852
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
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                                                                                                                                                                                                                                                                                                                                                                                     ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
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                                                                                                                                                                                                                                                                                                                  Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 192, Application US/09918715
; Sequence 192, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
RIOR PILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; RIOR PILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FRESEE for Windows Version 3.0
; SEQ ID NO 192
LENGTH: 500
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Pred. No. 1.5e-191;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.0
Matches 397; Conservative
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ORGANISM: Homo sapiens
   GENERAL INFORMATION
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US-09-918-715-192
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                                                                                                                                                                                                                                                                                                                            121 SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN
                                                                                                                                                                                                                                                                                                                                                     191 GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
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                                                                                                          1 ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                       Gaps
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Query Match 81.1%; Score 1799.5; DB 10; Lengt
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels
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APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
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CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PLING DATE: 2000-08-01
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SEQ THARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 297, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
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259 DAFMILNSSPEVPESQRRITETYHVELDSSKITTTSAVEFTPLPTCLQHQSCDTCVSSN 318
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                                                                                                                                                                       APPLICANT: Cargon-Walter, Eleanor
APPLICANT: Carcon-Walter, Eleanor
APPLICANT: Carcon-Walter, Eleanor
APPLICANT: Vogelstein, Bert
APPLICANT: Wogelstein, Bert
APPLICANT: Windler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR PLILING DATE: 2001-04-11
PRIOR PLLING DATE: 2001-04-11
PRIOR PLLING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FASELEG for Windows Version 4.0
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Publication No. US20040213793A1

GENERAL INFORMATION:
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Wogelstein, Bert
APPLICANT: Wogelstein, Bert
APPLICANT: Winzler, Kenneth
ITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
TITLE OF INVENTION: ENDOTHELIAL CELL
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80.7%; Pred. No. 2.2e-163;
tive 39; Mismatches 39;
                                                                                                                      Sequence 192, Application US/10474794; Publication No. US20040213793A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.79
Matches 331; Conservative
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US-10-474-794-192
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US-10-474-794-297
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APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFRENCE: 01-072-A
FILE REPRENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT APPLICATION NUMBER: 60/293,852
PRIOR APPLICATION NUMBER: 60/293,852
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 500
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 PONRTRVVEDNHNYYVSRVYGPGEKQSQDLWVDLAVANRSHVKIHRILSSSHRQASRVVL
                                                                                                           GTVFVVQWDHVYLQGWEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10156487A Publication No. US20030092025A1
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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Chids, John
APPLICANT: Chao, Cheng-Chi
APPLICANT: Mize, Nancy
APPLICANT: Lee, Juh;
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERRNCE: 30266,37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
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                                                                                                                                                                                                                                                                                                                                                                                295 TTSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVH 354
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                                                                                                                                            VVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKBIPMSVPBISSSQHP
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                      1 LAMDTLEPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
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                                                                   115 ASRVVLSFOFPFYGHPLROITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
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Pred. No. 4.8e-163;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 36, Application US/10168365; Publication No. US20030211987A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.9°
Best Local Similarity 94.2
Matches 343; Conservative
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US-10-168-365-36
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
RICH APPLICATION NUMBER: PCT/US00/35260
RICH APPLICATION NUMBER: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
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                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                       39; Indels
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Pred. No. 2.2e-163;
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ilarity 94.2%; Pred. No. 4.8e-163;
Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                       39; Mismatches
           CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SEQ ID NO 297
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09912935
Publication No. US20030022825A1
                                                                                                                                                                                                                                                                     81.1%;
80.7%;
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Best Local Similarity 80.77
Matches 331; Conservative
FILE REFERENCE: 1107.00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-36
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Best Local Similarity
Matches 343; Conserv
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ORGANISM: Mouse
                                                                                                                                                                                                                                  US-10-474-794-297
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Search completed: January 28, 2005, 22:19:20 Job time : 113.059 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

January 28, 2005, 21:55:58 ; Search time 7.47922 Seconds (without alignments) 1389.370 Million cell updates/sec

US-09-918-715-230_COPY_137_244 588 Title: Perfect score:

1 LSFDFPFYGHPLRQITIATG......LHHDGRIVFAYKEIPMSVPE 108 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	, QI	Description
-	317.5	54.0	476	7	T19786	hypothetical prote
7	123	20.9	1161	-	S31213	nidogen precursor
m	84	14.3	2120	~	T30243	alpha tectorin - c
4	83.5	14.2	1321	7	A60165	sodium channel pro
ιΩ	79	13.4	310	7	JC7853	L-fucose-specific
9		13.3	2155	7	T30197	alpha tectorin - m
7		12.4	1879	7	S74915	extracellular nucl
80	73	12.4		~	E71086	hypothetical prote
6	68	11.6		N	A97919	3-oxoacyl-{acyl-ca
10	68	11.6		~	C95048	3-oxoacyl-(acyl-ca
11	68	11.6	337	7	S77723	vitamin B12 recept
12	67.5	11.5		7	JH0289	class I histocompa
13	67.5	11.5		~	S18606	phosphoenolpyruvat
14	67	11.4		~	JC4553	heme dl synthesis
15	67	11.4		7	B82510	transporter, NadC
16	67	11.4	543	~	B64232	transport system p
17	67	11.4	614	П	ORECBT	vitamin b12 recept
18	67	11.4	614	~	A98241	
19		11.4	614	~	F86088	
20	99	11.2	330	7	H71981	
21		11.2	365	7	T08679	_
22	99	11.2	614	7	AB0935	vitamin B12 recept
23		11.2	728	7	S59964	procollagen-lysine
24	65.5	11.1	2214	7	T16305	hypothetical prote
25	65	11.1	362	7	JH0288	
		10.9	280	-	VPXRMN	outer capsid prote
27		10.9	280	-	VPXR16	o.
28	64	10.9	401	0	A85758	probable oxidoredu
29	64	10.9	401	,0	B64877	probable membrane

probable oxidoredu	pregnancy-specific	pregnancy-specific	reaction center co	reaction center co	outer layer protei	probable polyketid	cytochrome c oxida	conserved hypothet	lysine specific pe	glutamine-fructose	hypothetical prote	conserved hypothet	conserved hypothet	60S ribosomal prot	pregnancy-specific
D90861	B36109	A34595	A48290	T31454	VPXRW9	T28702	G97742	G89877	A86899	B72412	D71073	A95064	C97931	D90134	D33258
7	7	~	~	7	Н	~	7	0	N	~	~	~	~	~	7
401	424	424	609	609	176	1407	337	390	206	909	189	243	264	375	435
10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7
64	64	64	64	64	64	64	63.5	63.5	63.5	63.5	63	63	63	63	. 63
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

```
hypothetical protein C36E8.3 - Caenorhabditis elegans
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A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3 A;Experimental source: clone C36E8

A;Gene: CESP:C36E8.3

A;Map position: 3 A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2 C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Gaps ï Query Match

54.0%; Score 317.5; DB 2; Length 476;

Best Local Similarity 55.7%; Pred. No. 4.5e-26;

Matches 59; Conservative 19; Mismatches 27; Indels 1;

1,

9 1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 요 ð

61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106 :|:|||:| :| |: :|: ||||| || :| || ||: | 8 셤

RESULT 2

nidogen precursor - sea squirt (Halocynthia roretzi)
N.Alternate names: entactin
C;Species: Halocynthia roretzi
C;Species: Halocynthia roretzi
C;Accession: S31213
R;Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.
Bur. J. Biochem. 213, 11-19, 1993
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of c
A;Reference number: S31213; MUID:93238676; PMID:8477687

A,Molecule type: mRNA
A,Residues: 1-1161 <NAK>
A,Residues: 1-1161 <NAK>
C,Superfamily: Ascidian nidogen; ERF homology; LDL receptor YWTD-containing repeat homol C,Superfamily: Ascidian nidogen; EGF homology; LDL receptor YWTD-containing repeat homol C,Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu F;1-20/Domain: signal sequence #status predicted <SIG>

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A.Title: Nucleotide sequence of the putative sodium channel gene from Drosophila: the for A.Reference number: S04029; MUID:88040482; PMID:2444928
A.Accession: S04029
                                                                                                              A;Residues: 1-362;363-626;627-1321 <SAL>
A;Cross-references: UNIPROT:022930; EMBL:X14394
R;Salkoff, L.; Butler, A.; Wei, A.; Scavarda, N.; Giffen, K.; Ifune, C.; Goodman, R.; Mar Science 237, 744-749, 1987
A;Title: Genomic organization and deduced amino acid sequence of a putative sodium chann A;Reference number: A60165; MUID:87292090; PMID:2441469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 132-147;148-177 <1S2>
C,Comment: This protein, with ferrichrysin-affinity, has hemagglutination activity again
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding a fucose-specific le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: FlyBase:NaCP60E
A;Cross-references: FlyBase:FBgn0002920
A;Introns: 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1; 626/3; 751/2; 801/1; 908/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Aspergillus oryzae
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 09-Jul-2004
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 09-Jul-2004
C;Accession: 477853, PC719, Pata, Y.; Kawato, A.; Suginami, K.; Abe, Y.; Imayasu, S;Biosci. Biotechnol. Biochem. 66, 1002-1008, 2002
A;Title: Molecular cloning and overexpression of fleA gene encoding a fucose-specifyA;Reference number: 477853; MUID:22087106; PMID:12092808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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llarity 45.2%; Pred. No. 0.78;
Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 40-355;363-560,'P',562-626;632-1263 <8A2>
A;Cross-references: RWBL:XX4394
A;Note: part of this sequence was confirmed by mRNA sequencing
A;Note: the authors' translation is shown at position 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 NFNPGYSDNSTVVYFDN--GTVFVVQWDHVYLQGWEDKGSFT
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A;Residues: 1-310 <ISH>
A;Cross-references: UNIPROT:Q8TGE0; DDBJ:AB072379
A;Experimental source: strain OSI1018
A;Accession: PC7191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.2%; Score 83.5; DF
Best Local Similarity 31.1%; Pred. No. 1.5;
Matches 19; Conservative 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown A;Molecule type: DNA
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nes 19; Conserv
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Matches
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Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Odougaer, R.G.; Legan, P.K.; Richardson, G.P.
Ricoutinho, P.; Goodyaer, R.G.; Legan, P.K.; Richardson, G.P.
Hear. Res. 130, 62-74, 1999
A; Title: Chick alpha tectorin: molecular cloning and expression during embryogenesis.
A; Reference number: Z20783; MUID:99251817; PMID:10320099
A; Accession: T30243
A; Accession: T30243
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2120 < COU>
A; Residues: 1-2120 < COU>
A; Residues: 1-2120 < COU>
A; Cooss-references: UMIPROT:09YH85; EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAC
A; Note: non-collagenous protein only expressed in the inner ear
F;21-1161/Product: nidogen #status predicted <MAT>
F;274-306/Domain: BGF homology <EG1>
F;274-306/Domain: BGF homology <EG1>
F;560-574/Region: 3-realidue repeats (R-P-V)
F;660-574/Region: 3-realidue repeats (R-P-V)
F;603-673/Domain: thyroglobulin type I repeat homology <THY1>
F;686-748/Domain: thyroglobulin type I repeat homology <THY2>
F;752-819/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;944-986/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;944-986/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;1032-1075/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;107-1114/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;107-1114/Domain: EGF homology <FW5>
F;107-1114/Domain: EGF homology <FW5>
F;107-334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S04029; A60165
R;Salkoff, L.; Butler, A.; Scavrda, N.; Wei, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.9%; Score 123; DB 1; Length 116 Best Local Similarity 28.0%; Pred. No. 7.7e-05; Matches 40; Conservative 18; Mismatches 41; Indels
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hypothetical protein PH0954 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Accession: E71086
B;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
Rilegan, P.K.; Rau, A.; Keène, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A; Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com A; Reference number: 220771; MUID:97236843; PMID:9079715
A; Accession: T30197
A; Accession: T30197
A; Accession: T30197
A; Accession: T30197
A; Catus: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2155 ALBCA
A; Accession: T30197
A; Crosser-references: UNIPROT:008523; EMBL:X99805; NID:g1915908; PIDN:CAA68138.1; PID:g191
A; Experimental source: strain CD1; Whole cochleae
A; Note: non-collagenous protein only expressed in the inner ear, by cells both in and su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA A; Residues: 1-1879 «KIN» A; Residues: 1-1879 «KIN» A; Residues: 1-1879 «KIN» A; Cross-references: UNIPROT: P72938; EMBL: D90902; GB: ABB001339; NID: g1652027; PIDN: BAA1695 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extracellular nuclease - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein s110656
S;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74915
R;Kaneko, T; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
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A;Status: nucleic acid sequence not shown; translation not shown
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Best Local Similarity 26.34
Matches 31; Conservative
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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi M.) Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                    A;Residues: 1-4436 <KAW>
A;Residues: 1-4436 <KAW>
A;Cross-references: UNIPROT:058659; GB:AP000004; NID:g3236131; PIDN:BAA30051.1; PID:d103
A;Experimental source: strain OT3
A;Experimental sources strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) [imported] - Streptococcus pneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPROT: Q93NA1; GB: AE007317; PIDN: AAK99181.1; PID: g15457938; GSPDB: G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptococcus pneumoniae
C;Date: 22-Oct.2001 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
C;Date: 22-Oct.2001 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
C;Date: 22-Oct.2001 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
R;Accession: A97919
G;Accession: A97919
G;Accession: A7, Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; S., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; J. Y.; P.; Sun, P.M.; Winkler, M.B.
J; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Acteriol. 183, 5709-5717; MUID:21429245; PMID:11544234
A;Accession: A97919
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : | | : : | | : : | | 152 SDVIFGLDEDLATYDGYLLLVNLQDKIVIEWLASTYEDYESEIVDNINFQVIINSNGTIT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 LTAACSGFVF-----ALSTAEKFIA--SGRFQKGLVIGSETLSKAVDWSDRSTAVLFGD 159
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                                                                                                                                                    A;Accession: E71086
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSFDFFFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.4%; Score 73; DB 2; Length 4436; larity 17.8%; Pred. No. 84; Conservative 27; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 324;
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C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III
C;Keywords: acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
12;
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11.6%; Score 68; DB 3
Best Local Similarity 23.5%; Pred. No. 12;
Matches 31; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NGTVFVVQWDHVYLQGW-----EDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVFVV----QWDHVYLQGWEDKGS-
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FAIRDVAKSIKQ 231
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Best Local Similarity
Matches 23; Conserva
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A; Residues: 1-324 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: PH0954
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RESULT C95048

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20; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                             A; Residues: 1-356 < YUH>
                                                                                                                                                                                                                                            A;Molecule type: mRNA
                                                                                                                                                                                                              A; Accession: JH0289
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Best Local Simi
Matches 30;
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              Sylectes: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Accession: C95048
R; Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reterence number: A95000; MUID:21357209; PMID:11463916
A; Recension: C95048
A; Status: preliminary
A; Reseidues: 1-324 KUR>
A; Scatus: preliminary
A; Reseidues: 1-324 KUR>
A; Cross-references: UNIPROT:Q93NA1; GB:AE005672; PIDN:AAK74580.1; PID:g14971886; GSPDB:G
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: Sp0417
C; Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
S77723
vitamin B12 receptor - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S77723
R;Ward, R.J.; Glass, R.E.
Mol. Microbiol. 16, 813-815, 1995
A;Title: The 3'-terminal half of the btuB gene of Citrobacter freundii defines essential
A;Reference number: S77723
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-377 cWAR>
A;Residues: 1-377 cWAR>
A;Genetics:
C;Genetics:
A;Genetics:
C;Superfamily: vitamin B12 receptor; tonB-dependent receptor amino-terminal homology; tc
C;Keywords: membrane protein; vitamin B12 transport
F;85-337/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
3-oxoacyl-(acyl-carrier-protein) synthase III [imported] - Streptococcus pneumoniae (stq
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20.7%; Pred. No. 13;
ive 12; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 ITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPG----
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FAIRDVAKSIKQ 231
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RESULT 12

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C;Accession: JH0289
R;Yuhki, N.; O'Brien, S.J.
J. Exp. Med. 172, 621-630, 1990
A;Title: DNA recombination and natural selection pressure sustain genetic sequence diver A;Reference number: JH0288; MUID:90324882; PMID:1695669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: S18606
R,Osteras, M.; Finan, T.M.; Stanley, J.
R,Osteras, M.; Finan, T.M.; Stanley, J.
R,Osteras, M.; Finan, T.M.; Stanley, J.
A; Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encoding A; Reference number: S18606; MUID:92079905; PMID:1720862
A; Accession: S18606
A; Status: pre-liminary
A; Rocule type: DNA
A; Residues: 1-535 < OST>
                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:Q95485; GB:U07672; NID:g467252; PIDN:AAA19462.1; PID:g467253
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Fil-14 Domain: signal sequence (fragment) #status predicted <SIG>
Fil-14 Domain: signal sequence (fragment) #status predicted <MAT>
Fil9-108/Product: class I histocompatibility antigen #status predicted <MAT>
Fil9-108/Domain: alpha-1 <ALI>
Fil0-209/Domain: alpha-2 <ALI>
Fil0-297/Domain: alpha-3 <ALI>
Fil0-297/Domain: alpha-3 <ALI>
histocompatibility antigen precursor (clone FLA-B9) - cat (fragment)
                                C;Species: Felis silvestris catús (domestic cat)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Rhizobium sp.
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X63291
C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Keywords: carbon-carbon lyaes; carboxy-lyase; nucleotide binding; P-loop
F;234-241/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: spleen
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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F;324-356/Domain: intracellular #status predicted <INT>
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24.8%; Pred. No. 16;
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A;Cross-references: UNIPROT:Q51480; DDBJ:D50473; NID:g1217594; PIDN:BAA09066.1; PID:g121
A;Experimental source: RM31
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Pland, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Acadardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Setatus: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-462 - HEI>
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                   A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A,Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: H83581
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-39x <STO>
A;Cresiduess: EB:AE004488; GB:AE004091; NID:g9946372; PIDN:AAG03905.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A,Gene: nirF; PA0516
C,Superfamily: Pseudomonas stutzeri heme dl synthesis protein nirF
                                            heme d1 synthesis protein nirF - Pseudomonas aeruginosa
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A;Map position: 2
C;Superfamily: probable transporter MJ0672
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 31114, A Sequence 31114, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 250, App Sequence 250, App Sequence 250, App Sequence 250, App Sequence 250, App Sequence 250, App		TO STEM CELL GROWTH FACTOR-LIKE	Length 431; Indels 14; Gaps 3;	BEANKSQVKIHTILSNTHRQ 131 	COYVAPLMANFNEGYSDNST 191 	PRAYKEIPMSVPEISSSQHP 251 	MMSAVEFTPLPTCLQHRSCD 311
2 US-08-484-993B-18 2 US-08-484-158B-18 2 US-08-484-156A-18 3 US-08-480-150A-18 3 US-08-149-2731-18 6 5169835-6 4 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-252-991A-31114 US-09-573-986-9 4 US-09-461-255-50 4 US-10-012-542-550 4 US-10-012-542-550 4 US-10-012-542-550	ALIGNMENTS	LS RELATING DLYNUCLEOTID 35	; Score 2185; DB 4; ; Pred. No. 1.3e-209; 0; Mismatches 7;	LAMDTL.PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ 	ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST 	VVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEI 	VKTGLSDAFMILNDSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLOHRSCD
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28 30 31 31 31 32 33 34 34 34 34 34 34 34 34 34		RESULT 1 US-09-912-935-36 Sequence 36, Applicat. Recent No. 6673904 GENERAL INFORMATION: TITLE OF INVENTION: CURRENT APPLICATION IN PRIOR APPLICATION IN PRIOR PELLING DATE: NUMBER OF SEQ ID NOS SOFTWARE: PATENTIN NUMBER OF SEQ ID NOS CORGANISM: HOMO SED IN NOS CORGANISM: HOMO SED IS NOS	Query Match Best Local Sit Matches 416;	Oy 72 Db 1	Qy 132 Db 61	Qy 192 Db 121	Qy 252 Db 181

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Sequence 40, To Application US/09912935

Sequence 40, To Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

TITLE OF INVENTION: POLYMPEPTIDES AND POLYMUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.0

SEQ ID NO 40
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  POLYPEPTIDES AND POLYNUCLEOTIDES
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48.1%; Score 1295; DB 4;
Best Local Similarity 57.3%; Pred. No. 1.7e-120;
Matches 250; Conservative 72; Mismatches 106;
                   FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
FRIOR PPLICATION NUMBER: PCT/US00/35260
FRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 28
LENGTH: 529
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BPVG-EKEGFIVSEQC 529
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Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: POLVPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 499

    Sequence 28, Application US/09912935
    Patent No. 6673904
    GENERAL INFORMATION
    APPLICANTY: Nishikawa, Mitsuo et al.
    TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH PACTOR-LIKE

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48.1%; Score 1295; DB 4; Length 499;
Best Local Similarity 57.3%; Pred. No. 1.6e-120;
Matches 250; Conservative 72; Mismatches 106; Indels
                                                              484 VEPSCHEKEGFMEAEQC 500
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; ORGANISM: Homo sapiens
US-09-912-935-31
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US-09-912-935-31
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          DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD
                        VLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAEVEPSGHE
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                            ; Sequence 38, Application US/09912935; Patent No. 6673904; GENERAL INFORMATION:
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416 KEGFIVSEOC 425
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US-09-912-935-38
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US-09-912-935-38
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Matches 248;
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Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TILE STERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2000-10-24
NUMBER: POT SEQ 1D NOS: 53
SOFTWARE: Patentin version 3.0
SEQ 1D NO 35
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                                                                 72 LAMDTLPDNRTRVVED-NHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHR
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57.7%; Pred. No. 9.7e-119;
ive 64; Mismatches 106; Indels
                     Mismatches 106;
        Pred. No. 1.7e-120;
57.3%; FIL.
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248; Conservative
                     Conservative
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; ORGANISM: Homo sapiens
US-09-912-935-35
       Similarity
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US-09-912-935-35
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                                                                                                                                                                                                                                                                | GENERAL INFORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Tang, Y. T.
| APPLICANT: Childs, Cheng-Chi
| APPLICANT: Childs, John
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
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| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Methods and Materials Relating to No. 6667391el Methods and Methods an
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Length 392;
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                                                                                                                                                  US-09-764-325A-23; Sequence 23; Application US/09764325A; Patent No. 6667391; GENERAL INFORMATION:
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; Sequence 25, Application US/09764325A
; Patent No. 6667391
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ORGANISM: Homo sapiens
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US-09-764-325A-23
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Sequence 23, Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Mize, Cheng-Chi
APPLICANT: Chids, John
APPLICANT: Chids, John
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
TILE REFERENCE: 3026/37630A
CURRENT APPLICATION NUMBER: 09/547,358
FRIOR APPLICATION NUMBER: 09/547,358
FRIOR APPLICATION NUMBER: 09/545,714
FRIOR PILING DATE: 2000-04-11
FRIOR PILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 25
SEQ ID NOS: 25
SEQ ID NOS: 25
SEQ ID NOS: 25
FRIOR PLEATION OF SEC ID NOS: 25
FRIOR PILING DATE: 
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43.7%; Score 1176.5; DB 4
Best Local Similarity 58.6%; Pred. No. 7.6e-109;
Matches 229; Conservative 60; Mismatches 95;
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APPLICANT: Nightkawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 PVKVGLSDAFVVVHRIQQIPNVRRRIIYEYHRVELQMSKIINISAVEMTPLPTCLQFNRC
                       296 VEPTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRM
                                                                                                                                                                                                                                          411 -NNLSPKTKGTPVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPA
  KEIPMSVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 LAMDTLPDNRTRVVED-NHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTK 418
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                                                                                                                                                                                                                                                                                                                     470 MKFRSHPDHSTYAEVEPSGHEKEGFMEAEQC 500
                                                                                                                                                                                                                                                                                                                                            363 MKFRRGSGHPAYAEVEPVG-EKEGFIVSEQC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/09912935; Patent No. 6673904; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-912-935-34
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-912-935-34
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US-09-181-706-2
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APPLICANT: NIShikawa, Mitsuo et al.
TITLE OF INVENTION: METHORS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: METHORS AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PAPLICATION NUMBER: PCT/US00/35260
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 25
LENGTH: 392
                                                                                                                                                                                                                       116 RSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFFFMGDVIHRMLTATQYV 175
                                                                                                                                                                                                                                                                                                    235
                                                                                                                                                                                                                                                                                                                                          63 APLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGY 122
                                                                                                                                                                                                                                                                                                                                                                                  KEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSA 295
                                                                                                                                                                                                                                                                                                                                                                                                         123 KEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRM 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 VEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKEKM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEDFQDEDHDSASPDT--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 CENTEPVETSSRITITIGATITOFRVLITIRRAVISOFPISLPIEDDIKIALHLKDNGAS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 -NNLSPKTKGTPVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 RSQVKIHTILSNTHRQASRVVLSFDFPYGHPLRQITIATGGFIFMGDVIHRMLTATQYV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 APLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAY 235
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                                                                                                                                                                                                                                                                                                    176 APLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAY
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                                                                                                                                     43.7%; Score 1176.5; DB 4; Length 392;
.larity 58.6%; Pred. No. 7.6e-109;
Conservative 60; Mismatches 95; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

43.7%; Score 1176.5; DB 4; Length 392;
Best Local Similarity 58.6%; Pred. No. 7.6e-109;
Matches 229; Conservative 60; Mismatches 95; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKFRSHPDHSTYAEVEPSGHEKEGFMEAEQC 500
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-912-935-25
                                                                             , ORGANISM: Homo sapiens
US-09-912-935-23
                                                                                                                                                          al Similarity
229; Conserv
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                                                                                                                                       Query Match
Best Local S
Matches 229
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                                                          TYPE: PRT
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256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR-----R 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 194
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       310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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4.3%; Score 115.5; DB 3;
Best Local Similarity 20.6%; Pred. No. 0.086;
Matches 77; Conservative 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM PC compatible
CORRATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: WOR'D for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
RAPLICATION DATA:
APPLICATION DATA:
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2
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REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEPRAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henr
STREET: 51 University St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1569 amino acids
                                                                                                                                                                                                                                                                Sequence 2, Application US/09458791; Patent No. 6174689; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                 362 EDHDSASPDTSFSP 375
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                 516 KEKTTVTMVGSFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: WA
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVVM------NRTVLF 391
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APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION NUMBER: 26, 1998
CLASSIFICATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%; Score 115.5; DB 3; Length 1568; 20.6%; Pred. No. 0.086; ive 42; Mismatches 118; Indels 137;
Sequence 2, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. DuBose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMARHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: October 28, 1998 CLASSIFICATION:
                                                                                                                                                            CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
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Best Local Similarity 20.0%
Local 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / MOLECULE TYPE: protein US-09-181-706-2
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                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                  CITY:
STATE:
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423 TPV-----FYKLVPDP-----VKNIYIY------LTAGKEVRIRVANCNKHKS 460
                                                                                                                                                                                      461 CSECLTA-TDPHCGWCHSLQRCTFQGDCVHSENLENWLDI----SSGAKKCPKIQIIRSS 515
                                                                                                                                                        310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 LILSSSLVEALDVWAGVFSAAAGGGQERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS 94
                                                                 250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches 118; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEB: Janis C. Henry
SIRRET: 51 University St.
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.3%; Score 115.5; DB
Best Local Similarity 20.6%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC comparations of OPERATING SYSTEM: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word for Windows 95, 7. (CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/459,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09459065
Patent No. 6562949
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                               362 EDHDSASPDTSFSP 375
                                                                                                                                                                                                                                                                             516 KEKTTVTMVGSFSP 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1568 amino acids
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3Y: linear
                       392 LGTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98101
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                                                                                                                                                                                                                                                                                                                                                                                  US-09-459-065-2
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250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS 309
                                          423 TPV-----FYKLVPDP-----VKNIYIY------LTAGKEVRRIRVANCNKHKS 460
                                                                                      310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                                GAATGWPSMAR-----IAQSTEVLFQGQASLDCGHGH------PDGR------R 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NRTVLF 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 1568;
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                                                                                                                                                                                                                                                                                                                     Security 200-2
Patent No. 6187909
GENERAL INFORMATION:
APPLICANT: STIGGS, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.3%; Score 115.5; DB 3;
20.6%; Pred. No. 0.086;
iive 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 26.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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516 KEKTTVTMVGSFSP 529
                                                                                                                                                                           362 EDHDSASPDTSFSP 375
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TYPE: amino acid
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US-09-459-066-2
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Best Local Similarity
Matches 77; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: WA
COUNTRY: US
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353 HCKEGDQPERVQPIASSTLIHSDLTSV-YGTVVMNRTVLF 391	195 FDNGTVFVVQWDHVYLQGWEDKGSPTFQAALHHDGRIVFAYKEIPMSVPEISSSQ 249	392 LGTG	HRIELDPSKVTSMSAVEFTPLPTC	423 TPVFYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKS 460	310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQD 361	461 CSECLTA-TDPHCGWCHSLQRCTFQGDCVHSBNLENWLDISSGAKKCPKIQIIRSS 515	362 EDHDSASPDTSFSP 375	516 KEKTTVINVGSFSP 529
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Search completed: January 28, 2005, 22:14:18 Job time : 42.8779 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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January 28, 2005, 21:55:58; Search time 34.626 Seconds (without alignments) 1389.370 Million cell updates/sec Run on:

US-09-918-715-230
2691
1 MRGELWLLVLVLREAARALS.....YAEVEPSGHEKEGFWEAEQC 500

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	å Query Match Length	DB	ΩI	Description
	- 5		20.7	•	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	111111111111111111111111111111111111111
7	110	7.77	7	4	113/00	ingportiented proce
61	126	4.7	1161	-	S31213	nidogen precursor
e	115.5	4.3	1568	~	T09074	semaphorin recepto
4	103.5	3.8	979	~	C86446	probable cellulose
Ŋ	101.5	3.8	743	~	T09173	EH domain protein
9	101	3.8	733	~	E86345	hypothetical prote
7	100	3.7	535	~	S18606	phosphoenolpyruvat
8	66	3.7	1133	~	T12529	hypothetical prote
σ	86	3.6	345	~	T16074	hypothetical prote
10	98	3.6	1502	7	S45429	probable membrane
11	97	3.6	708	~	183196	NEDD-4 ORF - mouse
12	96.5	3.6	397	7	S33415	corticosteroid-bin
13	96.5	3.6	619	7	T19703	hypothetical prote
14	95.5	3.5	399	Н	S71480	homeotic protein H
. 15	95.5	3.5	887	~	S70642	ubiquitin ligase N
16	95.5		2120	~	T30243	alpha tectorin - c
17	94	3.5	774	~	JC7265	neprilysin (EC 3.4
18	93.5		979	Н	JC2349	protein-tyrosine-p
19	93.5		966	~	148721	PTP 35 protein - m
20	93.5	•	1977	7	S54771	sodium channel alp
21	93		491	7	AG3506	phosphoenolpyruvat
22	93	٠	1085	7	855352	IFH1 protein - yea
23	92.5	3.4	441	7	JC7653	pectate lyase (EC
24	92.5	3.4		7	A85041	probable receptor
25	91.5	3.4	614	7	A98241	
26	91.5	3.4		~	F86088	hypothetical prote
27	91.5	3.4		Н	P2WMBB	2a protein - broad
28	91.5	3.4	1042	7	A57534	mucin 5AC (clone L
29	91	3.4	633	7	S47144	mating type A prot

protein-tyrosine-p	pregnancy-specific	zona pellucida gly	pristinamycin I sy	phosphoenolpyruvat	phosphoenolpyruvat	hypothetical prote	protein tyrosine p	hypothetical prote	hypothetical prote	protein-tyrosine k	Doc4 protein, stre	pregnancy-specific	osteonidogen - hum	probable polyketid	sodium channel pro
S51005	JN0067	870399	T30289	AD2581	B97363	T25104	I58345	T05673	T51491	T30200	T14271	A34595	G00043	T03222	CHRTM1
~	~	~	~	~	~	7	~	7	7	7	~	7	~	~	-
1175	332	424	4848	561	561	798	1176	1179	1189	1621	2825	424	1376	1762	1840
3.4	3.4	3.4	3.4	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3
. 91	90.5	90.5	90.5	90	90	06	90	90	06	06	90	89.5	89.5	89.5	89.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 T19786 hypothetical C;Species: C3 C;Date: 15-0c C;Accession: R;MlKinson, R;MlKinson, R;A;Rcession: R;Rcference I A;Rcference I A;Rcfe	RESULT 1 T19786 Pypothetical protein C36E8.3 - Caenorhabditis elegans C;Species: Genorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T19786 A;Wilkinson, J; Barlow, K. Swilkinson, J; Barlow, K. Swilkinson, J; Barlow, K. Swilkinson, T19786 A;Reference number: Z19177 A;Reference number: Z19177 A;Reserius: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-76 cWIL> A;Residues: 1-76 cWIL> A;Residues: 1-76 cWIL> A;Residues: CWILPROT:018500; EMBL:Z35597; FIDN:CAA84646.1; GSPDB:GN00021; CESP:C3 A;Experimental source: clone C36E8 C;Genetics: C;Genetics: C;Genetics: A;Rap position: 3 A;Rap position: 3 A;Rap position: 3 A;Rap position: 3 A;Introns: Z3/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2 C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3
Query M Best Lo Matches	Query Match 22.7%; Score 611; DB 2; Length 476; Best Local Similarity 34.2%; Pred. No. 5.6e-42; Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;
y da	46 RRARESPGHVSEPDRTQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPS 100
ζς Q	101 EPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATG 156
yo da	157 GFIFMGDVIHRMLTATQYVAPLMANFNPGXSDNSTVVYFDNGTVFVVQMDHVYLQGWEDK 216 ::
S qa	217 GSFTFQAALHHDGRIVFAXKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRR 274
o, qa	275 RSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLT-FNCSWCHVLQR 330
ço Qo	331CSSGFDRYRQEWMDYGCAQEAEGRMCE-DFQDEDHDSAS-PDTSFSPYDGDLTTTS 384
ζζ	385 SSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTIVGIVLAVLLVAAIILAG 444 409 LPLDADKWKKTDKTTSEDSDEWKGHKKKEEPK

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mxNA
A;Residues: 1-1568 <CCM>
A;Residues: 1-1568 <CCM>
A;Cross=references: UNIPROT:060486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3
A;Experimental source: tissue type foreskin; cell type fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CjAccession: C86446
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q9FVR3; GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 TPV------FYKLVPDP------YKNIYIY------LTAGKEVRRIRVANCNKHKS 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSECLTA-TDPHCGWCHSLORCTFOGDCVHSENLENWLDI----SSGAKKCPKIQIIRSS 515
                                                                                                                                                                                                                                                                                                                                                                                                                         95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 LILSSSLVEALDVWAGVFSAAAGEGGERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 HCKEGDOPERVOPIASSTL------IHSDLTSV-YGTVVM-----NRTVLF 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 LGTG------DGOLLKVILGENLTSNCPEVIYEIKEE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DPPPYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 194
                                                                                                                                                                                                                                                                                                                          39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQL
                                                                                                                                                                                                                                                                                                                                                                GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR-----
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                                                                                                                                                                                                                         Length 1568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 979;
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21.2%; Pred. No. 5.2;
tive 48; Mismatches 167;
                                                                                                                                                                                                                                             20.6%; Pred. No. 1,
tive 42; Mismatches 118;
                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                              4.3%; Score 115.5;
                                                                                                                             C;Genetics:
A;Gene: VESPR
C;Keywords: receptor; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 EDHDSASPDTSFSP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 21.2%
Matches 87; Conservative
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEKTIVIMVGSFSP
                                                                                                                                                                                                                                                  Local Similarity
ses 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-979 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                                                                                                                           Query Match
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Matches
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Afittle: A poxvirus-encoded semaphorin induces cytokine production from monocytes and kareference number: 216555; MUID:98246049; PMID:9586637
                                                                                                                                                                                                                                                                                                                                                 shuffling two kinds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 DIFFREHKDNATIARANTDVREAFIETAGDFNAGSVFVVTWDKVQSASREDGVTFTFQCI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 LSFDFPFYGHPLROITIATGGFIFM-----GDVIHRMLTATQYVAPLMAN----- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 --FNPGYSDNSTVVY-------FDNGTVFVVQWDHVYLQGWEDKGSFTFQAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHHDGRIVFA---YKEIPMSVPEIS----SSQHPVKTGLSDA----FMILNPSP----DV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 PESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------HVKK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nidogen precursor - sea squirt (Halocynthia roretzi)
N;Alternate names: entactin
C;Species: Halocynthia roretzi
C;Bpecies: Halocynthia roretzi
C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S31213 #sequence_revision 7.; Endo, T.; Obinata, T.
R;Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.
Bur. J. Blochem. 213, 11-19, 1993
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling twanterence number: S31213; MUID:99238676; PMID:8477687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         semaphorin receptor VESPR - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 AGSQGQWIFQIGGIMFNNDEASKESE-----KH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 126; DB 1;
23.5%; Pred. No. 0.094;
tive 34; Mismatches B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 RCSSGFDRYRQEW-MDYGCAQEAE-GRMCEDF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 TROSGPOVSEVNFNEDFNIDLEAECGTPCSDF 281
                                        445 IYINGHP--TSNAALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 23.5
nes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S31213
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19;

Gaps

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosicules: 1-345 <GET-
A;Mosicules: 1-345 <GET-
A;Cross-references: UNIPROT: Q19446; EMBL: U28737; NID: G860717; PID: G860723; PIDN: AAA68276
A;Experimental source: strain Bristol N2
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C;Species: Saccharomyces cerevisiae
C;Species: Saf529; S4520; S4520; S5226
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
A;Description: Sequence analysis of a 78,6 kb segment of the left end of Saccaromyces ce, A;Reference number: S45387
A;Accession: S45429
A;Accession: S45429
A;Accession: S4522
A;Coss-references: UNIPROT: P38181; EMBL:X79489; NID:G496661; PID:G496702
                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 PLPTCLOHRSCDACMSSDLTPNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GDVNPD-DCSYYDHPISTTWSP-------NTQCSASAEN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPVHLGTIVGIVLAVLLVAAIIL-----AGIY------INGHPTSNAALFF 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 TYFWLMISFAIIIAILAILLILULLELCCGLFTGRQSARRSEDGDWIVPKTPKANHELYD 282
      AFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTC-LQHRSCDACMSSD 317
                                                                                                                                  318 LIFNCSWCHVLORCSSGFDRYRQEWMDYGC------AQEAEGRMCEDFQDEDH 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F14B8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 LTATI --NRKCNG--ADQYGFNCN----EQCST----VNNDYYCYTCGSNGQKTCCAS-
                                                                  937 AMLOADDEDDLMEERMKSPF-----GSSFRTFNATDYKPIATIDVKRNIFDLCTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 MSVPEISSSCHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFT
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                                                                                                                                                                                                                                                                                                     probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                             365 DSASPDISFSPYDGDLTTISSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R,Geisel, C. submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid F14B8. A;Reference number: Z18456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
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3.6%; Score 98; DB 2
Best Local Similarity 18.7%; Pred. No. 3.4;
Matches 50; Conservative 46; Mismatches
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                                                                                                       encodin
                                                                                                    pckA of Rhizobium NGR234,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 -----DKGSFTFQAALHHDGRIVFAYKEI------PMSVPEISSSQ---HPVKTGLSD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877 AIHKEDKFNMNISGVFHPNGLEVIINTEIWDLRTFHLLHTVPALDQCRVVFNHTGTVMYG 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTLAMDT----LPDNRTRVVED-----NHSYYVSRLYGPSEPHSRELWVDVAEANRSQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDQIWWDNNSAISPENFERLRODMLAHAKGMSLYVQDLVGAGQSGK-----CVADARRHR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TGGFIFMGDVIHRMLTATQYVAP-----1MANFNPGYSDNSTVVYF----- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 VKIHTI-LSNTHRQASRVVLS-----FDFP-FYGHP--------LRQITIA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 IRWHSLFIRNLLIRPPREGLASFLPKLTIIDLPSFKANPERHGCRGETIIACDLTKGLVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 -DNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 VERPLGRSLQLRAABLYEE----AFARRGALTAHGALCARTGQHTGRSPKDKYVVRDAAT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHV--SEPDRTQLSQDLG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 VMENVVLDERRAPDFDNG---SLTENTRIAYPLDFIPNASETGTAPQPRTIIMLTADA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 GLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein DKFZp434P113.1 - human (fragment)
hypothetical protein DKFZp434P113.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Ju1-1999 #sequence_revision 23-Ju1-1999 #text_change 09-Ju1-2004
C;Accession: T1529
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
C;Accession: S18606
R;Osteras, M.; Finan, T.M.; Stanley, J.
Mol. Genet. 230, 257-259, 1991
Mol. Genet. 230, 257-259, 1991
A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NG A;Ritle: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NG A;Reference number: S18606; MUID:92079905; PMID:1720862
A;Recession: S18606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <OST>
A;Cross-references: EMBL: X63291
C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Superfamily: phosphoenolpyruvate carboxy-lyase; nucleotide binding; P-loop F;234-241/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDIAH--IYDIQTGNKLLTLFNPDLANN----YKRNCATFNPTDDLVLNDGVLWDVRSAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.7%; Score 100; DB 2; Length 535; Best Local Similarity 19.8%; Pred. No. 4.3; Matches 71; Conservative 50; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7%; Score 99; DB 2; Length 1133; 23.0%; Pred. No. 15; tive 37; Mismatches 119; Indels
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1133 <WAM>
A;Residues: 1-1133 <WAM>
C;Croserreferences: UNIPROT:09UG37; EMBL:AL080145
A;Experimental source: adult testis; clone DKFZp434P113
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Best Local Similarity
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A,Note: DKFZp434P113.1
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C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui
F;40-77/Domain: WW repeat homology <WWl>
                                                                                                                                                                                                                                                    F;196-233/Domain: WW repeat homology <WW2>
F;251-288/Domain: WW repeat homology <WW3>
F;347-682/Domain: ubiquitin-protein ligase homology <UBI>
       A; Reference number: 160167; MUID: 92328780; PMID: 1378265
                                                                                                          A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetics:
                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 EPD----
                                                                                                                                                                                 A; Gene: NEDD-4
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                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1262-1502 <CON>
A;Cross-references: EMBL:235840; MIPS:YBL079w
A;Experimental source: strain $288C
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
Yeast 11, 1103-1112, 1995
A;Title: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevis
A;Reference number: $59184; MUID:96076635; PMID:7502586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X79489; NID:g496661; PIDN:CAA56029.1; PID:g496702
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLLRDIWGRHVFM-TFTDNRV----TSHAFISSS--DPITPSINNLKSDEISQNRNII- 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IHTILSNTHRQASRVVLSFD-FPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAP-L 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SKVSISKDCIEYY---LSSINILNEFFITYGDSI-----SQISAPYV 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANFNPGYSDNSTVVYFD-----NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
A,Experimental source: strain $288C

Ribomdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.

Rubmitted to the Protein Sequence Database, August 1994

A,Reference number: $45816

A,Accession: $45810

A,Accession: $45810

A,Residues: 1-1502 < DOM>
A,Reference: Strain $288C

R;Contreras, R.; Fiers, W.; Logghe, M.; Molemans, F.

R;Contreras, R.; Fiers, W.; Logghe, M.; Molemans, R.
A,Reference number: $45802

A,Accession: $45802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%; Score 98; DB 2; Length 1502; Best Local Similarity 22.7%; Pred. No. 26; Matches 62; Conservative 41; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;231-247/Domain: transmembrane #status predicted <TM1>F;434-450/Domain: transmembrane #status predicted <TM2>F;764-780/Domain: transmembrane #status predicted <TM3>F;1311-1327/Domain: transmembrane #status predicted <TM4>F;13182-1399/Domain: transmembrane #status predicted <TM4>F;1382-1399/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1406-1423/Domain: transmembrane #status predicted <TM6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: SGD:S0000175; MIPS:YBL079w A; Map position: 2L
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corticosteroid-binding globulin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: 833415; 843740
R;Scrocchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L.
R;Scrocchi, L.A.; 903-90; 1999
A;Title: Spatial and temporal distribution of corticosteroid-binding globulin and its me A;Reference number: 833415; MUID:93145908; PMID:7916682
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A;Residues: 1-397 <SCR1>
A;Cross-references: UNIPROT:Q06770; EMBL:X70533; NID:g298114; PIDN:CAA49934.1; PID:g2981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 VFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESR-RRSIFEYHRIELDPSKV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 TSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 AEGRMCEDFQDE---DHDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDTKL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 LKARLWIEFDGEKGLDYGGVAREWFFLISKEMFNPYYG------LFEYSATDNYTLQI 398
                                                                                                                                                                                                                                                                                                                                                                                                   72 SPDDDLTDEDNDDMQLQAQRAFTTRRQISEDVDG-----PDNRESPENWEIVREDEN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYYVSR-LYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDF----PFY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 TEYSGQAVQSPPSGH----IDV-----IDV------QTH------IAEFFNTRLAVC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM----ANFNPGY----SDNSTVVYFD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 GNPATSQPVTSSNHSSRGGSLQTCIFEEQPTLPVLLPTSSGLPPGWEEKQDDRGRSYYVD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------LRRANILEDSYRR-IMGVKRADL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 NGTVFVVQWDHVYLQ----------GWEDKGSFTFQAALHHDGRI 231
                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                            14 EAARALSP-----QPGAG----HDEGPG---SGWAAKGTVRG----WNRRARESPGHVS 56
                                                                                                                                                                                                                                      DOAEBLEPGWVVLDOPDAATHLPHPPEPSPLPPGWEBRODVLGRTYYVNHESRRTQWKRP 71
                                                                                                                                                                                                                                                                                                                         ----RTQLSQDLGGGTLAMDTLPDNRTR-----VVEDNH
                                                                                  Indels 186;
3.6%; Score 97; DB 2; Length 708; 19.4%; Pred. No. 11;
                                                                              51; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TDIPNKFEMK----
                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 23-40 <SCR2>
C;Superfamily: Serpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S43740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S33415
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NEDD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: 183196
C;Accession: 183196
R;Kunar, S.; Tomooka, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression

C;Keywords: glycoprotein; steroid binding F;1-22/Domain: signal sequence #status predicted <sig> F;23-397/Product: corticosteroid-binding globulin #status experimental <mat> F;89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status predicted</mat></sig>	Qy 302 P 302 1 586 P 586
Query Match Best Local Similarity 20.2%; Pred. No. 5.5; Matches 53; Conservative 47; Mismatches 104; Indels 59; Gaps 11;	
Qy 61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEA 114	homectic protein Hox B3 - chicken C;Species: Gallus gallus (chicken) C;Abte: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S71480
115 NRSQVXIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHR	R;Scotting, P.J.; Rex, M. Submitted to the EMBL Data Library, August 1993 A;Reference number: S71480 A;Accession: S71480
OY 168 MLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFT 220	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1.399 <sco> A;Cross-references: UNIPROT:P23682; EMBL:X74506; NID:g398704; PIDN:CAA52613.1; PID:g4437</sco>
221 FQAALHHDGRIVPAYKEIF : ::: 269 VVAALNRDTIDRWGKLMIP-RQM	C;Genetics: A;Gene: Hox-B3 C;GenerEmily: homeotic protein Hox B3; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation P;160-216/Domain: homeobox homology <hox></hox>
Oy 270 PESRRSIFEYHRIELDPSKV 290 DD 328 TKDTPLTLTVLHKAMLQLDEGNV 350	Query Match 3.5%; Score 95.5; DB 1; Length 399; Best Local Similarity 20.5%; Pred. No. 6.7; Matches 62; Conservative 40; Mismatches 110; Indels 91; Gaps 10;
היה אינה אינה אינה אינה אינה אינה אינה א	Qy 246 SSSQHPVKTGLSDAFMILNPSPDVPBSRRSIFEYHRIELDPSKVTSMSAVEFT 299
Appointment procession: Carlotte elegans Cispectes: Canorhabditis elegans Cispectes: Canorhabditis elegans Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 Cispectesion: T19703	300 PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWM
Alreference number: Z19166 Alreference number: Z19166 Alreference number: Z19166	344 DYGCAQEAEGRACEDFQDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTT
A; Molecule Cype: DNA A; Residues: 1-679 <wil> A; Cross-references: UNIPROT: Q09495; EMBL: Z46996; PIDN: CAA87102.1; GSPDB: GN00021; CESP: C3 A; Experimental source: Q1one C34C12</wil>	395 EDDTKLAPYAGEDGLONNLSPKTKGTPVHLGT 1
C;Genetics: A;Gene: CESP:C34C12.2 A;Map position: 3 A;Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3	Qy 427 IVGIVLAVLLVAAIILAGIYINGHPTSNAALFPIERRPHHWPAMKFRSHPDHSTYAEVEP 486
Query Match 3.6%; Score 96.5; DB 2; Length 679; Best Local Similarity 23.3%; Pred. No. 12; Matches 70; Conservative 36; Mismatches 130; Indels 65; Gaps 12;	Qy 487 SGH 489
	RESULT 15 Sylotata ubiquitin ligase Nedd4 - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S70642 R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. EMBO J. 15, 2371-2380, 1996 A;Title: Ww domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(+) A;Recession: S70642 A;Recession: S70642 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-887 cSTA> A;Cross-references: UNIPROT:Q62940; EMBL:US0842; NID:g1293646; PIDN:AAB48949.1; PID:g129 C;Genetics: A;Gene: Nedd4 C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui

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90 SYYVSR-LYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPL 148
                                                                                                                                                                                                                                                                                                                                                                                                                            : | : : | | : : | | : | 330 IIXSGQAVQSPPSGHP-DVQVRLAB-----ELDTRLT-------MYGNPA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 RQITIATGGFIFMGDVIHRMLTATQYVAPLM----ANFNPGY----SDNSTVVYFDNGTV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 AYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESR-RRSIFEYHRIELDPSKVTS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 INHNİKKTQWEDPRMQNVAITG------PAEPYSRDYKRKYEFFRKLKKQ---- 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 MSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 DOAEELEPGWVVLDQPDAATHLQHPPEPSPLPPGWEERQDVLGRTYYVNHESRTTQWKRP 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 TSQPVTSSNHSSRĞGSSQTCIFEEQPTLPVLLPTSSGLPPGWEEKQDDRGRSYYVDHNSK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 FVVQWDHVYLQ------GWEDKGSFTFQAALHHDGRIVF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 GRMCEDFQDE---DHDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDT-KLN 401
                                                                                                                                                                                                                       14 BAARALSP-----OPGAG---HDEGPG---SGWAAKGTVRG-------WNRR 47
                                                                                                                                                                                                                                                                                                            48 ARES------VVEDNH 89
                                                                                                                               Query Match 3.5%; Score 95.5; DB 2; Length 887; Best Local Similarity 19.2%; Pred. No. 20; Matches 93; Conservative 55; Mismatches 155; Indels 181;
F;54-167/Domain: protein kinase C C2 region homology <KC2> P;246-283/Domain: WW repeat homology <WW1> P;402-439/Domain: WW repeat homology <WW3> P;459-496/Domain: WW repeat homology <WW3> P;555-881/Domain: wbiquitin-protein ligase homology <UBI>
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PNSG 612
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Search completed: January 28, 2005, 22:12:46 Job time : 36.626 secs THIS PAGE BLANK (USPTU)

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January 28, 2005, 21:59:20 ; Search time 136.657 Seconds (without alignments) 1321.880 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2000-08-01
PRIOR PLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PLILING DATE: 2000-08-11
PRIOR PLILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTHARE: PRESERG for Windows Version 3.0
LENGTH: 500

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		0; Gaps	VSEPDR	VSEPDR	NRSQVK
	500;	ö	ESPGH	ESPGH	DVAEA
	Length	Indels	RGWNRRAR	RGWNRRAR	SPHSRELWV
	DB 10;	, 647-9 , 0	WAAKGT	WAAKGT	RLYGPSI
TYPE: PRT ORGANISM: Homo sapiens 9-918-715-230	100.0%; Score 2691; DB 10; Length 500;	best bocal Similatily 100.0%; Fied. NO. 4.96-249; Matches 500; Conservative 0; Mismatches 0; Indels	MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGW	1 MRGELWILVLVIREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR 60	61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYORLYGPSBPHSRELWVDVAEANRSQVK 120
TYPE: PRT ORGANISM: HOMC -09-918-715-230	Query Match	Matches 50(1	г	61

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241 SVPEISSSQHPVKTGLSDAFWILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP 300
241 SVPEISSSQHPVKTGLSDAFMILNPSPDVFSRRRSIFEYHRIELDPSKVTSMSAVEFTP 300
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                                                    SVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP
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| Sequence 230, Application US/10474794
| Publication No. US20040213793A1
| GENERAL INFORMATION:
| APPLICANT: Carson-Walter, Eleanor
| APPLICANT: Carson-Walter, Eleanor
| APPLICANT: St. Croix, Brad
| APPLICANT: Kinzler, Kenneth
| TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
| FILE REFERENCE: 1107.00179
| CURRENT PLILING DATE: 2003-10-14
| PRIOR PLILING DATE: 2001-04-11
| PRIOR PLILING DATE: 2001-04-01
| NUMBER: OF SEQ ID NOS: 359
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: SOO
                                                                                                                                                                                                                                                                                                                                                       181 YAEVEPSGHEKEGFMEAEQC 500
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US-10-474-794-230
                   181
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GENERAL INCRAMATION:

APPLICANT: Wirez, Ralph
APPLICANT: Kallabls, Haarald
TITLE OF INVENTION: BREYONTION BREYONDSIS

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
FILE REFERENCE: LeA 36 108
CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT APPLICATION NUMBER: EP03003112.4
PRIOR PILING DATE: 2003-05-09
PRIOR PILING DATE: 2003-05-13
PRIOR PILING DATE: 2003-05-11
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PATENTION NUMBER: BP02010291.9
FRIOR PILING DATE: 2002-05-21
SOFTWARE: PATENTION NUMBER: BP02010291.9
FRIOR PILING DATE: 2002-05-21
SOFTWARE: PATENTION NUMBER: BP02010291.9
FRIOR PILING DATE: 2003-05-05-21
SOFTWARE: PATENTION NUMBER: BP02010291.9
FRIOR PILING DATE: 2002-05-21
SOFTWARE: PATENTION NUMBER: BP02010291.9
FRIOR PILING DATE: 2003-05-21
SEQ ID NO 79
FRIOR PILING DATE: 2003-05-21
SEQ ID NO 79
FRIOR PILING DATE: 2003-05-21
SEQ ID NO 79
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                                     IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA 180
                                                           SVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP 300
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   TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
                                                                                                          NFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
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100.0%; Pred. No. 4.9e-249;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 79, Application US/10435696
Publication No. US20040018525A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 500; Conservative
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US-10-435-696-79
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US-10-435-696-79
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                                                                                                       1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
                                                   Gaps
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100.0%; Score 2691; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1.4e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 0;
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  DB 17; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
CURRENT APPLICANTON UNMBER: US/09/918,715
CURRENT APPLICATION UNMBER: 2001-08-01
PRIOR APPLICATION UNMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
                                                   Indele
100.0%; Score 2691; DB 17;
llarity 100.0%; Pred. No. 4.9e-249;
Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-918-715-179
                           Best Local Similarity
Matches 500; Conserv
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APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Main G.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-5384
CURRENT APPLICATION NUMBER: 09/520,781
PRIOR APPLICATION NUMBER: 09/584,411
PRIOR PILING DATE: 2000-05-31
PRIOR PILING DATE: 2000-05-31
PRIOR PLING DATE: 2001-02-14
PRIOR PILING DATE: 2002-02-25
PRIOR PILING DATE: 2002-02-25
PRIOR PILING DATE: 2002-02-12
PRIOR PILING DATE: 2002-02-12
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PRIOR PILING DATE: 2002-02-13
                                                                                                                                                                                                         361 DEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT 420
     LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ 360
                                                                                                       DEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT
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NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                              481 YAEVEPSGHEKEGFMEAEQC 500
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Patturajan, Meera
Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Shimkets, Richard A.
Spytek, Kimberly A.
Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10357819
Publication No. US20040259774A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alvarez, Enrique
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Ji, Weichen
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, Li
Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-10-357-819-2
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LENGTH: 500
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APPLICANT: Shenger, Janiel K.
APPLICANT: Shenger, Janiel K.
APPLICANT: Shency, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spyrek, Kimberly A.
APPLICANT: Spyrek, Kimberly A.
APPLICANT: Edoug, Wei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21002-538A
CURRENT APPLICATION NUMBER: US/202, 781
PRIOR PELLING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 09/584,411
PRIOR APPLICATION NUMBER: 09/584,411
PRIOR APPLICATION NUMBER: 09/783,436
PRIOR FILING DATE: 2000-02-13
PRIOR PELING DATE: 2002-02-25
PRIOR PELING DATE: 2002-02-25
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                                                                                      NENPGYSDNSTVVYFDNGTVFVVQMDHVYLQGMEDKGSFTFQAALHHDGRIVFAYKEIPM 742
                                                                                                                                                                                                                                             PVHLGTIVGIVLAVLLVAAIILLAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHST 480
NFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
                                                                                                                                                                                                                          LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alvarez, Enrique
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
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Rieger, Daniel K.
Shenoy, Suresh G.
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Ji, Weizhen
Kekuda, Ramesh
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Miller,
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                                                                      TQLSQDLGGGTLAMDTLPDDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 622
                                                                                                                           121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA 180
                                                                                                                                                623 IHTILSNIHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA 682
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        503 MRGELWILVLVLVREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR 562
                                             TOLSODLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSOVK 120
                                                                                                                                                                                                                                                                                                                       743 SVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP 802
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Bublication No. US20040213793A1

GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: Carson-Walter, Eleanor

APPLICANT: Vogelstein, Bert

APPLICANT: Kinzler, Kenneth;

TITLE OF INTENTION: ENDOTHELLAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

CURRENT FILING DATE: 2003-10-14

PRIOR PELICATION NUMBER: 60/282,850

PRIOR PELICATION NUMBER: 60/380,829

PRIOR APPLICATION NUMBER: 60/308,829

PRIOR PELICATION NUMBER: 2001-04-11

PRIOR PELICATION NUMBER: 2001-06-01

NUMBER OF SEQ ID NOS: 359

SOCTUMENT: SESSEQ for Windows Version 4.0

SEQ ID NO 179
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llarity 100.0%; Pred. No. 1.4e-248;
Conservative 0; Mismatches 0;
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US-10-474-794-179
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Best Local S
Matches 500
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ORGANISM:
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GENERAL INFORMATION:
APPLICANT: Juan, Todd
APPLICANT: Juan, Todd
APPLICANT: Oliner, John
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT PILING DATE: 2002-09-10
PRIOR PILING DATE: 2002-09-10
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 502
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PRIOR APPLICATION NUMBER: 60/359,367
PRIOR FILING DATE: 2002-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 4
LENGTH: 488
                                                                                                                                                                                                      12;
                                                                                                                                                                      Length 488;
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                                                                                                                                                                      Score 2602; DB 17;
Pred. No. 1.7e-240;
1; Mismatches 0;
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Best Local Similarity 97.4%;
Matches 487; Conservative
                                                                                                                         : Homo sapiens
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CORGANISM: Homo sapiens
US-10-156-487A-5
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; ORGANISM: HC
US-10-357-819-4
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APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPREBNCE: 1107.00134
CURRENT APPLICATION NUMBER: 06/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
Score 2566; DB 14; Length
Pred. No. 5e-237;
0; Mismatches 7; Indels
     Length
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Best Local Similarity 81.6%; Pred. No. 9.6e-203;
Matches 409; Conservative 46; Mismatches 44;
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Query Match
Best Local Similarity 95.9%;
Matches 487; Conservative
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KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM 179
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                                   240 MSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFT 299
                                                                                                                                                                       300 PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDF 359
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                 KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM 179
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APPLICANT: Juan, Todd
APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Oliner, John
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT FILING DATE: 2002-09-10
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SSG ID NO 6
FORMARY: PALENT OF TURE APPLICATION NUMBER: 06/293,852
NUMBER OF SEQ ID NOS: 15
SSG ID NO 6
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                                                   RIQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQV 119
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MSVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFT
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Sequence 297, Application US/09918715

Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Bard St. Croix

APPLICANT: Bard St. Croix

APPLICANT: Reneth Kinller

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REPERENCE: 1107.00134

CURRENT FILING DATE: 2000-08-01

PRIOR PILING DATE: 2000-08-02

PRIOR PILING DATE: 2000-08-11

SEQ ID NO 297

SEQ ID NOS: 358

SEQ ID NO 297
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81.6%; Pred. No. 9.6e-203;
iive 46; Mismatches 44;
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; ORGANISM: Mouse
US-09-918-715-297
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US-09-918-715-297
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Best Local S
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241 MAVLDISSAQHPVKAGLSDAFMILNSSPEVPESQRRTIFEYHRVELDSSKITTTSAVEFT 300
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                   120 KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFWGDVIHRMLTATQYVAPLM
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82.1%; Score 2209; DB 17
Best Local Similarity 81.6%; Pred. No. 9.6e-203
Matches 409; Conservative 46; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                      EXPRESSION
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Kinzler, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESS.
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR PILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: PSESCE FOR WINDOWS VERSION 4.0
SEQ ID NO 297
LENGTH: 500
                                                                                                                                                                                                                                                  Sequence 297, Application US/10474794; Publication No. US20040213793A1; GENERAL INFORMATION:
                                                                                                                                                                  480 TYTEVEPSGHEKEGFVEAEQC 500
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US-10-474-794-297
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                                                    PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAGRMCEDF 359
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APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Winzler, Kenneth
ITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 359
SEQ ID NOS: 359
SEQ ID NOS: 359
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81.6%; Pred. No. 9.6e-203;
iive 46; Mismatches 44;
                                                                                                                                                                                                                                                      TYAEVEPSGHEKEGFMEAEQC 500
                                                                                                                                                                                                                                                                       ; Sequence 192, Application US/10474794; Publication No. US20040213793A1; GENERAL INFORMATION:
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Matches 409; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-474-794-192
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APPLICANT: Mize, Nancy
APPLICANT: Lee, Juhi
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES
FILE REFRERNCE: 3026/37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 431
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                                                                                                                                                                                                                                                                                            Length 431;
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95.2%; Pred. No. 1.5e-200;
iive 0; Mismatches 7;
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Job time : 138.657 secs
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Chao, Cheng-Chi
Drmanac, Radoje T
Mize, Nancy
Lee, Juhi
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Best Local Similarity 95.2
Matches 416; Conservative
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TITLE OF INVENTION: METHODS AND MATRIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLECTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2010-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0 . .
SOFTWARE: Patentin version 3.0 .
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                   TYAEVEPSGHEKEGFMEAEQC 500
                                     US-09-912-935-36
Sequence 36. Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/10168365; Publication No. US20030211987A1; GENERAL INFORMATION:
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Best Local Similarity 95.2
Matches 416; Conservative
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Childs, John
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ORGANISM: Homo sapiens
US-09-912-935-36
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

January 28, 2005, 21:52:02 ; Search time 158.818 Seconds (without alignments) 1129.372 Million cell updates/sec

US-09-918-715-230

score: Perfect sc Sequence:

1 MRGELWLLVLVLREAARALS......YAEVEPSGHEKEGFMEAEQC 500

BLOSUM62

Scoring table:

2002273 seqs, 358729299 residues Searched:

Gapop 10.0 , Gapext 0.5

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	Description	Abb90749	Abu54456	Adi21063	Adh13230	Adi21554	Adi21553	Abb90723	Abu54430	Adi21064	Abb90783	Abb90729	Abu54436	Abu54490	Aab85400	Abo01434	Aab43131	Aab85396	Abo01430	Aab85394	Abb90734	Abb90726	Abp53349	Abg69157	Abg69161	Abu54441
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SUMMAKIES	01	ABB90749	ABU54456	ADI21063	ADH13230	ADI21554	ADI21553	ABB90723	ABU54430	ADI21064	ABB90783	ABB90729	ABU54436	ABU54490	AAB85400	AB001434	AAB43131	AAB85396	ABO01430	AAB85394	ABB90734	ABB90726	ABP53349	ABG69157	4BG69161	ABU54441
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	Query Watch Length	500	200	200	200	527	527	1002	1002	488	200	200	200	200	431	431	400	499	499	529	529	529	529	529	529	529
dŧ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.96	82.1	82.1	82.1	82.1	81.2	81.2	74.6	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1
	Score	2691	2691	2691	2691	2691	2691	2691	2691	2607	2209	2209	2209	2209	2185	2185	2007	1295	1295	1295	1295	1295	1295	1295	1295	1295
	Result No.	-	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu54433 Human tum Abo01436 Human ste Abo01428 Human ste Aae35354 Human TEM Adn05749 Antipsori Aab31211 Amino aci Aau29259 Human PRO Am39668 Human pol Abu58635 Human PRO Abu88183 Novel hum Abu8498 Human sec Abr65762 Human sec Abr65762 Human sec Abu85762 Human sec Abu82941 Human sec	Novel Human Novel Human
ABU54433 ABO01428 ABO01428 AAN05749 AAN129259 AAN39068 ABU58635 ABU88183 ABR66372 ABR65762 ABR65762 ABR65762 ABR65762 ABR65762 ABR659999999999999999999999999999999	ABU90062 ABR68311 ABU96364 ABU92795 ABO08872
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4 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4	4444 12844 10845

ALIGNMENTS

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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                         Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.
             ABB90749 standard; protein; 500 AA
                                           (first entry)
                                                                                                                                  WO200210217-A2.
                                                                                                                   Homo sapiens
                                           30-MAY-2002
                                                                                                                                                07-FEB-2002.
                                                                                                      psoriasis.
                            ABB90749;
RESULT 1
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01-AUG-2001; 2001WO-US024031.

02-AUG-2000; 2000US-0225599P. 11-AUG-2000; 2000US-0224360P. 11-APR-2001; 2001US-0282850P.

(UYJO) UNIV JOHNS HOPKINS.

ä Vogelstein St Croix B, Kinzler KW,

WPI; 2002-291856/33.

N-PSDB; ABL92103

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.

Claim 1; Page 206-207; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB907569. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic

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retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL921996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                               TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
                                                                                                                                                                                                                                                                                TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSBEPHSRELWVDVAEANRSQVK 120
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                                                                                                                                                                                                                                                                                                                           IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; pc; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; neoangiogenesis; immune response; cytostatic; antidiabetic, ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                                                                                                         100.0%; Score 2691; DB 5; Length 500; 100.0%; Pred. No. 3.1e-249;
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                                                                              (PEM) ABL91903-ABL91995
                                                                                                                                                         Similarity
                                                                                                          Sequence 500 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 NFNPGYSDNSTVVYYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIFM 240
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                                                                                                                                                                                               designated as tumor endothelial
                                                                                                                                                                                             New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                             The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tummour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are all useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducting an immune response to tumour endothelial cells in a patient, for identifying candidate durys for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
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                                                                                                                 Kinzler KW, Vogelstein
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100.0%; Pred. No. 3.1e-249;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                 Disclosure; Page 221-222; 374pp; English
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10-APR-2002; 2002WO-US008253
                             11-APR-2001; 2001US-0282850P.
06-FEB-2002; 2002US-0354262P.
                                                                                UYJO ) UNIV JOHNS HOPKINS
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Matches 500; Conservative
                                                                                                                 Carson-Walter E, St
                                                                                                                                                WPI; 2003-093016/08.
N-PSDB; ABX72028.
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polypeptide are useful in diagnostics, forensics, gene mapping, polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elloit immune response. The polypeptides are useful for raising antibodies is markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or respensation, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
                                                                                                                                                                         forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; myence; actilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J;
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Weng G, Zhou P, Drmanac RT,
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100.0%; Pred. No. 3.1e-249;
iive 0; Mismatches 0;
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                                 ADI21063 standard; protein; 500 AA
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2001; 2001US-0323739P.
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                                                                                                         entry)
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500; Conservative
                                                                                                                                           Novel human protein #38.
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Ghosh M, Xue AJ, W
Haley-Vicente D;
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N-PSDB; ADI21779.
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                                                                                                                                                                                                                                                                                                                  Predicting, diagnosing or prognosing malignant neoplasia by detecting at least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
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                                                                                                        NFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
                                                                                                                                                           241 SVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRKSIFEYHRIELDPSKVTSMSAVEFTP
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                                                                                         NFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
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                                        IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA
                                                         IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA
                                                                                                                                             SVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP
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bladder cancer; non-small cell lung cancer; human.
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13-FEB-2003; 2003EP-00003112.
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N-PSDB; ADH13207.
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19-SEP-2001; 2001US-0323739P. 19-SEP-2002; 2002WO-US029964

WO2003025148-A2 Homo sapiens

27-MAR-2003

(HYSE-) HYSEQ INC

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cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia such as breast cancer, ovarian cancer, gastric cancer, colon cancer, oesophageal cancer, mesenchymal cancer, pladder cancer or non-small cell lung cancer. The polymucleotides and polypeptides defined in the specification, antisense polymucleotides targeting the polymucleotides and compounds identified by the screening methods are useful for preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia. The disease di numan malignant neoplasia.
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                                                                                                                                                                                                                                                                                                      100.0%; Score 2691; DB 8; Length 500; 100.0%; Pred. No. 3.1e-249;
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                 Sequence 500 AA;
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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating mythoid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or egeneration, in wound healing in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
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                                                                                                                                                                                                                                                                                                                                      New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
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Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 527;
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Sequence 527 AA;
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11-AUG-2000;
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                      PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHST 480
                                                                                                          PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFIERRPHHWPAMKFRSHPDHST 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; none cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
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Weng G, Zhou P, Drmanac RT, Wang D;
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Wehrman T,
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13-SEP-2002; 2002US-00323739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptide #32.
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N-PSDB; ADI21333.
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Haley-Vicente D;
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                                                                                                                                                                                                                                 208 NFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
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                                                                                                                                                                                                  TOLSODLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK
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                                                 Indels
100.0%; Score 2691; DB 7;
100.0%; Pred. No. 3.3e-249;
ive 0; Mismatches 0;
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                                                                                                                             The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90749, ABB90713, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rate TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92041, and pan-endothelial markers
                                                                                                                                                                                                                                                                                                                                                                                               562
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                                                        An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                                                                                                                                                            Score 2691;
                                                                                                       Disclosure; Page 125-128; 331pp; English
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            Vogelstein
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ABU54430 standard; protein; 1002 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New purified human transmembrane protein, designated as tumor endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (PEM), normal polymucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
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                                                                                                          pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necoangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                         tumour endothelial cell;
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100.0%; Pred. No. 9e-249;
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Human tumour endothelial marker TEM 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lynucleotides and secreted proteins, useful for treating myeloid or id disorders, in bone cartilage, tendon, ligament and nerve growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                        forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang J;
Wang D;
                                                                                                                                                           LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ
                                                               DEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT
                                                                                                                     DEDHOSAS PDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT
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Drmanac 1
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3 G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 315; 156pp; English.
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shrman T, Weng G,
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                                                                                                                                                                                                                                                                                                                        ADI21064 standard; protein; 488
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2002US-00323739.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                Novel human protein #39.
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Ghosh M, Xue AJ, W
Haley-Vicente D;
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N-PSDB; ADI21780.
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normal endothelial marker; pan-endothelial marker; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                     1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
                                                                                                                                                                                                                                                         TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK
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                                                                                                                                                                                                                                                                                              121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA
                                                                                                                                                                                                                                                                                                               IHTILSNTHROASRVVLSFDFPFYGHPLROITIATGGFIFMGDVIHRMLTATQYVAPLMA
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                                                                                                                                                                                                                                                                                                                                                                      NFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
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                                                                                                                                                                                                                                                                                                                                                                                                              SVPEISSSQHPVKTGLSDAFMILNPSPDVPBSRRRSIFEYHRIELDPSKVTSMSAVEFTP
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                                                                                                                           Score 2607; DB 7;
Pred. No. 3.5e-241;
0; Mismatches 0;
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Similarity 97.6%;
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein;
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                                                                                                  Sequence 488 AA;
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                                                                                                                           Query Match
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                                                                                                                                              monse;
                                                                                                                                                                                                                  Mus musculus
                                                                                             30-MAY-2002
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                                                                                                                                                                                             psoriasis.
                                                                      ABB90729;
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                                                                                                                                             Human;
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                                                                                                                                                                                                                       variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90749, ABB90749, ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92191; normal endothelial markers (TEM) ABL91995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRGELWLL-VLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                           An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                  The invention relates to an isolated molecule comprising an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                           82.1%; Score 2209; DB 5; Length 5
81.6%; Pred. No. 6.7e-203;
ive 46; Mismatches 44; Indels
                                                                                                                                                                                         Disclosure, Page 301-302; 331pp; English.
                                                                                  Vogelstein B;
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          02-AUG-2000; 2000US-0225599P.
11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
                                                         (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 81.6
409; Conservative
                                                                                  Kinzler KW,
                                                                                                         2002-291856/33.
                                                                                                                    N-PSDB; ABL92136
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 500 AA;
                                                                                  Croix B,
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90749, ABB90732, ABB90732, ABB90732, ABB90732, ABB90730, and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endochelial markers (TEM) ABL92042-ABL92041, and pan-endothelial markers
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                                                                                                                                                                                                                                                                  TEM; tumour endothelial marker; NEM; PEM; cytostatic;
                                                                                                                                                                                                                                                                                               normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
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81.6%; Pred. No. 6.7e-203;
iive 46; Mismatches 44;
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ABB90729 standard; protein; 500
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified human transmembrane protein, designated as tumor endothelia marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                ANFNPGYSDNSTVAYFDNGTVFVVQWDHVYLQDREDRGSFTFQAALHRDGRIVFGYKEIP
                                                                  PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDF
                                                                                                              QDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKG
                                                                                                                                                            TPVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHS
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                                                       MSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFT
                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour anglogenesis; neoangiogenesis; immune response; cytostatic; antidiabetic, ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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06-FEB-2002; 2002US-0354262P.
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polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are aluseful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, for identifying candidate drugs for treating tumours. The present sequence represents a mouse TEM protein
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Pred. No. 6.7e-203;
46; Mismatches 44;
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; Pred. No. 6.7e-203.
46; Mismatches 44.
                                                                                                                                                              Kinzler KW,
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06-FEB-2002; 2002US-0354262P
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The invention provides novel human stem cell growth factor-like polypeptides and polymclectides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polymcleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzhaimer's disease. They may also be utilized to generate new tissues and organs that may aid spatients in need of transplants. They can also be used as nutritional supplements. The present sequence represents a tumour endothalial marker of precursor protein, homologous to a stem cell growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                    Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degemerative disease; Alzheimer; Alzheimer; cytostatic; nootropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; tumour endothelial marker 7 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVYFDNGTVEVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMDTL PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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Pred. No. 1.1e-200;
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                                                                                                                                                                       endothelial marker 7 precursor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
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TYTEVEPSGHEKEGFVEAEQC 500
                                                                            protein; 431
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                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
07-APR-2000; 2000US-00545714.
11-APR-2000; 2000US-00547358.
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95.2%;
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                                                                                                                                          (first entry)
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                                                                            AAB85400 standard;
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                                                                                                                                                                                                                                                                                                                 WO200153500-A1.
                                                                                                                                          17-SEP-2001
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                                                                                                           AAB85400;
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VKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New stem cell growth factor-like polypeptides and polynucleotides, useful for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis, graft-versus-host disease, cancers, Alzheimer's disease, Huntington's
VVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHP 180
                                                                                                                                                               ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEW-MDYGCAQEAEGRMCEDFQD-----ED 363
                                                                                                                                                                                                                     294
                                                                                                                                                                                                                                                                                                                TTSASPDISFSPYDGDLTTTSSSLFIDSLTTBDDTKLNPYAGGDGLQNNLSPKTKGTPVH 354
                                                                                                                                                                                                                                                                                                                                                                                     LGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAE 483
                                                                                                                                                                                                                                                                                                                                                                                                                    LGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAE 414
                                                                                                                                                                                            VKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCD
                                                                                                                                                                                                                                                                        HDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial marker 7 precursor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB001434 standard; protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEPSGHEKEGFMEAEQC 500
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DRMANAC R T.
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(CHAO/)
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The invention relates to a new isolated polypeptide, which has stem cell growth factor-like activity. The new polypeptide, the polymucleotide encoding this polypeptide, or the agonist of the polypeptide are useful for treating a subject in need of enhanced activity or expression of stem cell growth factor-like polypeptide. The antagonist of the polypeptide or

Example 4; Fig 2; 98pp; English.

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the activity or expression of stem cell growth factor-like polypeptide. The new polypeptide or polymucleotide is particularly useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types. In particular, the polypeptide or polymucleotide is useful for treating leukaemia, haemophilia, osteoporosis, osteoarthritis, anaemia, tendonitis, carpal tunnel syndrome, autoimmune diseases (e.g. multiple sclerosis, systemic lupus erythematosus, graft-versus-host disease or allergies), cancers or degenerative disease (e.g. Alzheimer's sclerosis) or for generating new tissues and organs that may aid patients in need of transplanted tissues. The polymucleotide may also be used in gene therapy for the treatment of these diseases. The new polypeptide or polymucleotide is also useful in diagnostic or research methods. The present sequence represents the human tumour endothelial marker 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEW-MDYGCAQEAEGRMCEDFQD-----ED 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWDGTMGCAQEAEG-----QDVRGLPGMRT 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 TISASPDISFSFYDGDLTITISSSLFIDSLITTEDDIKLNPYAGGDGLQNNLSFKTKGTFVH 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
polynucleotide is useful for treating a subject in need to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMDILEPDINETRVVEDINHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNDGYSDNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                               72 LAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 HDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKINPYAGGGGLQNNLSPKTKGTPVH
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Pred. No. 1.1e-200;
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Matches 416; Conservative C
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07_INBW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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-474 -474	US-09-918-715-193	-09-918	0-156-487A-	11-478	US-10-474-794-193	4-794-29	US-10-487-421-2	US-09-912-935-23	US-09-912-935-25	7-1	-168-365-2	US-09-912-935-35	65-3	US-09-912-935-34	US-10-168-365-34	US-09-912-935-31	US-10-168-365-31	15-	19-918-715-	US-09-912-935-28	9-912-	US-10-052-586-472	US-10-066-500-128	US-10-174-590-472	US-10-176-758-472	US-10-175-737-472	4	US-10-176-483-472	US-10-176-749-472
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14	16	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Spytek, Kimberly A.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/357,819
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR APPLICATION NUMBER: 09/544,411
PRIOR APPLICATION NUMBER: 09/544,411
PRIOR APPLICATION NUMBER: 09/783,436
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 10/085,198
PRIOR FILLING DATE: 2002-02-25
PRIOR PRILING DATE: 2002-02-25
              Sequence 4, Application US/10357819 Publication No. US20040259774A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Patturajan, Meera
Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Shimkets, Richard A.
Spytek, Kimberly A.
                                                                                                                                                                                                                                                                                                       Miller, Charles E.
Padigaru, Muralidhara
                                                                                                             Edinger, Shlomit R. Gangolli, Esha A. Gerlach, Valerie L. Gorman, Linda Guo, Weizhen Ji, Weizhen Kekuda, Ramesh
                                                                                      APPLICANT: Alvarez, Enrique
                                                                                                                                                                                                                                                                                        Li, Li
Miller,
JS-10-357-819-4
                                                                                                                                                                                          APPLICANT
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PRIOR FILING DATE: 2002-02-01

PRIOR PLING DATE: 2002-02-09

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR PLICATION NUMBER: 60/356,424

PRIOR PLICATION NUMBER: 60/358,239

PRIOR PLICATION NUMBER: 60/358,608

PRIOR PLING DATE: 2002-02-20

PRIOR PLING DATE: 2002-02-21

PRIOR PLING DATE: 2002-02-21

PRIOR PLING DATE: 2002-02-21

PRIOR PLING DATE: 2002-02-25

PRIOR PLING DAT
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Sequence 230, Application US/09918715

Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Bard St. Croix

APPLICANT: Bert Vogelstein
APPLICANT: Renneth Kinzler

TITLE OF INVEWTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134

CURRENT FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: 60/224,599
PRIOR PILICATION NUMBER: 60/224,360

PRIOR PILING DATE: 2000-08-02

PRIOR PILING DATE: 2000-08-01

NUMBER: OF SEQ ID NOS: 358

SOFTWARE: FESTE 2000-04-11

NUMBER: OF SEQ ID NOS: 358

LENGTH: 500

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Best Local Similarity 100.0%; Pred. No. 1.8e-36;
Matches 65; Conservative 0; Mismatches 0;
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Best Local Similarity 100.v
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US-10-357-819-4
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RESULT 3

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Sequence 79, Application US/10435696

Sequence 79, Application US/10435696

Sequence 79, Application US/10435696

Sequence 79, Application No. US20040018525A1

GENERAL INFORMATION:
APPLICANT: Witter, Rallabis, Harald

APPLICANT: Kallabis, Harald

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

FILE REPERENCE: Lepo3003112.4

PRIOR APPLICATION NUMBER: EP02010291.9

PRIOR PILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 314

SEQ ID NO 79

LENGHARE: PatentIn version 3.1

SEQ ID NO 79

MATERIAL SOOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 230, Application US/10474794
| Publication No. US20040213793A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Carson-Walter, Eleanor
| APPLICANT: Carson-Walter, Brad
| APPLICANT: Wogelstein, Bert
| APPLICANT: Kincler, Kenneth
| TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
| FILE REFRENCE: 1107.00179
| CURRENT APPLICATION NUMBER: US/10/474,794
| PRIOR PILING DATE: 2001-04-11
| PRIOR FILING DATE: 2001-04-11
| PRIOR FILING DATE: 2001-08-01
| NUMBER OF SEQ ID NOS: 359
| SEQ ID NO 230
| LEASTERN SOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 370; DB 15;
Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 65; Conservative 0;
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ORGANISM: Homo sapiens
US-10-474-794-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-10-435-696-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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1 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR 60
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100.0%; Score 370; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0;
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            GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Renneth Kinzler
TITLE OF INVENTION: BNOOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107. 00134
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,599
PRIOR PILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
STOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORATION:
CHARLAL INCORATION:
CHARLAL INCORATION:
APPLICANT: Carson-Walter, Bleanor
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 179, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
Sequence 179, Application US/09918715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-10-474-794-179
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-5384
CURRENT APPLICATION NUMBER: US/10/357,819
PRIOR PILING DATE: 2003-02-03
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2001-02-14
PRIOR PLING DATE: 2001-02-14
PRIOR PLING DATE: 2002-02-25
PRIOR PLING DATE: 2002-02-02
PRIOR PLING DATE: 2002-02-04
PRIOR PLING DATE: 2002-02-04
PRIOR PLING DATE: 2002-02-05
PRIOR PLING DATE: 2002-02-05
PRIOR PLING DATE: 2002-02-02
PRIOR PLING DATE: 2002-02-02
PRIOR PLING DATE: 2002-02-02
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NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
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100.0%; Score 370; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0
                                                                                                               Sequence 2, Application US/10357819
Publication No. US20040259774A1
GENERAL INFORMATION:
                                                                                                                                                                                                    APPLICANT: Alvarez, Enrique
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gornan, Linda
APPLICANT: Guo, Xiaojia
APPLICANT: Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li, Li
Miller, Charles B.
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Shimkets, Richard A.
Spytek, Kimberly A.
Zhong, Mei
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                                                                                                                                                                                                                                                                                                                                                                                                                             Kekuda, Ramesh
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ORGANISM: Homo sapiens
US-10-357-819-2
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QEWMD 344
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LENGTH: 500
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842 QEWMD 846

RESULT 6 US-09-918-715-179

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280 YHRIELDPSKVTSMSAVEPTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR 339
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                                                                                                                                       APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Oliner, John
TITLE OF INVENTION: Tunor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT FILING DATE: 2002-09-10
PRIOR FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
97.0%; Score 359; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 0; Mismatches 0;
                           Sequence 5, Application US/10156487A publication No. US20030092025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 502
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CRGANISM: Mus musculus
US-09-918-715-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-10-156-487A-5
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APPLICANT: Tang, Y. Tom
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, John
APPLICANT: Chids, John
APPLICANT: Chao, Cheng-Chi
APPLICANT: Dramac, Radoje T
APPLICANT: Lee, Juhi
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPRENCE: 30266/37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
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CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
                                                                                                                                   APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: POLYMETIDES AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYMETIDES AND POLYMUCLEOTIDES
TITLE OF INVENTION: POLYMETIDES AND FOLYMUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: DCT/US00/35260
PRIOR PILING DATE: 2000-12-23
SOFTWARE: PLANG DATE: 2000-12-23
SOFTWARE: PLANG DATE: 2000-12-23
SOFTWARE: PLANG DATE: 2000-12-23
SOFTWARE: PATENTIAN APPLICATION NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIAN APPLICATION APP
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                           Sequence 36, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 63; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-168-365-36
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JS-09-912-935-36
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Pred. No. 5.7e-31;
                                                                                     US-10-47-794-192

US-10-47-794-192

Sequence 192, Application US/10474794

Publication No. US20040213793A1

GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: Vogelstein, Bert

APPLICANT: Vogelstein, Bert

APPLICANT: Vogelstein, Bert

APPLICANT: Wogelstein, Bert

APPLICANT: Winzler, Kenneth

TITLE OP INVENTION: ENDOTHELLAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR PILING DATE: 2001-04-11

PRIOR PILING DATE: 2001-04-11

PRIOR PILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 192
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Best Local Similarity 84.4%;
Matches 54; Conservative
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Best Local Similarity 84.44
Matches 54; Conservative
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                      341 QEWL 344
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Publication No. US20
GENERAL INFORMATION:
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Sequence 6, Application No. US20030092025A1

GENERAL INFORMATION:

JAPPLICANT: USAN, Toold

APPLICANT: Dass, Michael B.

APPLICANT: Oliner, John

TITLE OF INVERTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof

FILE REFERENCE: 01-072-A

CURRENT APPLICATION NUMBER: US/10/156,487A

CURRENT PILING DATE: 2002-09-10

FRIOR APPLICATION NUMBER: 60/293,852

FRIOR APPLICATION NUMBER: 60/293,852

FRIOR APPLICATION NUMBER: 2001-05-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

LENGTH: 500
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84.4%; Pred. No. 5.7e-31;
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84.4%; Pred. No. 5.7e-31;
ive 7; Mismatches 3; Indels (
                                                                                                      Sequence 297, Application US/09918715
Sequence 297, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad & E. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Renneth Kinzler:
TITLE OP INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERRNCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT PILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-01
PRIOR PPLICATION NUMBER: 60/224,360
PRIOR PPLING DATE: 2000-08-01
PRIOR PLING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 297
LENGTH: 500
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Best Local Similarity 84.4
Matches 54; Conservative
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Matches 54; Conservative
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341 QEWL 344
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341 QEWL 344
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US-09-918-715-297
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Pred. No. 5.7e-31;
7; Mismatches 3; Indels (
GENERAL INFORMATION:

APPLICANT: Cargon-Walter, Eleanor

APPLICANT: Cargon-Walter, Brad

APPLICANT: Cargon-Walter, Brad

APPLICANT: Wogelstein, Bert

APPLICANT: Kinzler, Kenneth

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: 60/282,850

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR FILING DATE: 2001-04-11

PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359

SEQ ID NOS: 359

SEQ ID NOS: 359

LENGTHARE: FastsEQ for Windows Version 4.0

SEQ ID NO 297

LENGTH: 500
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61 QEWM 64 |||: 341 QEWL 344

Search completed: January 28, 2005, 22:19:19 Job time: 18.7655 secs

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NEDD-4 ORF - mouse
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protein-tyrosine-p
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sodium channel alp
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2: pir2:*
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A, Refer	rence numb	per: Z1	9177				
A; Accet	BSION: TIX	7/86	trana	u T	d from GB.	from CB/RMRI/DDBJ	
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A; Exper	s-reterenc rimental a	Ses: UN	IIPROT:(385	E8	EMBL:Z35597; FIDN:CAA84646.1; GSFDB:GNUUZI; C	CESP: CS
C, Genet	tics:				!		
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A;Introns: 23/1; 101/3; 152/3; 206/3; 2 C;Superfamily: Caenorhabditis elegans h	ons: 23/1; rfamily: C	aenorh	, 152/: abditi	3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	206/3; 235, elegane hypo	235/1; 255/3; 320/1; 445/2 hypothetical protein C36E8.3	
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È	200 GB	SFTFOAA	LHHDGR.		VKEIPMSVPI	GSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRR 257	
ф	235 HS	SFTFOTI	LHKNGD.	[VF]	YKOVPYDIS	NHPVKLGISDA	
ò	258 RS	3 I FEYHR	IELDPSI	ST.S	MSAVEFTPL	SIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLT-FNCSWCHVLQR 313	
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 11-Uun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09074
Immunity B, 473-482, 1998
A;Titles: A poxylius-encoded semaphorin induces cytokine production from monocytes and b A;Accession: T09074
A;Accession: T09074
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nidogen precursor - sea squirt (Halocynthia roretzi)
NyAlternate names: entactin
C;Species: Halocynthia roretzi
C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S31213
R;Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.
Blur, J. Blochem. 213, 11-19, 1993
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of A;Reference number: S31213; MUID:93238676; PMID:8477687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHHDGRIVFA---YKEIPMSVPEIS----SSQHPVKTGLSDA----FMILNPSP----DV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HVKK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 LSFDFPFYGHPLRQITIATGGFIFM------GDVIHRMLTATQYVAPLMAN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
5.7%; Score 126; DB 1; Length 1161;
Best Local Similarity 23.5%; Pred. No. 0.059;
Matches 64; Conservative 34; Mismatches 88; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AGSQGQWIFQIGGIMFNNDEASKESE-----KH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 RCSSGFDRYRQEW-MDYGCAQEAE-GRMCEDF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 TROSGFOVSEVNFNEDFNIDLEAECGTPCSDF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               semaphorin receptor VESPR - human
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A,Cross-references: UNIPROT:060486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3 A,Experimental source: tissue type foreskin; cell type fibroblast C,Genetics: A,Genetics: A,Genetics: C,Keywords: receptor; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ### domain protein Reps1 - mouse

NyAlternate names: RalBP1-associated EH domain protein Reps1

C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09173

R;Yamaguchi, A.; Urano, T.; Goi, T.; Feig, L.A.
A;Title: An eps homology (EH) domain protein that binds to the ral-GTPase target, RalBP1
A;Reference number: Z16602; MUID:980800; PMID:9395447
A;Accession: T09173
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A;Cross-references: UNIPROT:054916; EMBL:AF031939; NID:g2677842; PIDN:AAB94736.1; PID:g2
A;Experimental source: cell line: C2C12; tissue type: muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 LILSSSLVEALDVWAGVFSAAAGEGGERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF---- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------DGOLLKVILGENLTSNCPEVIYEIKEE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 TPV-----FYKLVPDP-----VKNIYIY------LTAGKEVRRIRVANCNKHKŚ 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 HCKEGDOPERVOPIASSTL------IHSDLTSV-YGTVVM------NRTVLF 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
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                                                                                                                                                                                                                                                                                                                                              GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
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                                                                                                                                                                                                                                                                                                                                                                                                        256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR-----
                                                                                                                                                                                                                                                                             Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 177;
                                                                                                                                                                                                            Length 1568;
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                                                                                                                                                                                                         Query Match 5.2%; Score 115.5; DB 2; Best Local Similarity 20.6%; Pred. No. 0.67; Matches 77; Conservative 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEKTTVTMVGSFSP 529
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A;Residues: 1-743 <YA
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Qy 196 WEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMIL 246 : : : : : : :	RESULT 6 S18606 plosphoenolpyruvate carboxykinase (ATP) (BC 4.1.1.49) - Rhizobium sp. C;Species: Rhizobium sp. C;Species: Rhizobium sp. C;Accession: S18606 R;Octeras, M.; Finan, T.M.; Stanley, J. Mol. Gen. Genet. 230, 257-269, 1991 A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, A;Recession: S18606 A;Molecule type: DNA A;Residues: 1-535 cOST> A;Cross-references: EMBL:X63291 C;Superfamily: phosphoenolpyruvate carboxykinase [ATP] C;Superfamily: phosphoenolpyruvate carboxy-lyase; nucleotide binding; P-loop F;234-241/Region: nucleotide-binding motif A (P-loop)	Query Match Best Local Similarity 20.7%; Pred. No. 3.5; Best Local Similarity 20.7%; Pred. No. 3.5; Matches 59; Conservative 39; Mismatches 117; Indels 70; Gaps 61 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTI-LSNTHR	OY 191 VYLGAWED/SESTIFQAALHHOSTIVFATKEIPMYVELUSSQHVYNTGELSDAFMILMESF 250	RESULT 7 T12529 hypothetical protein DKFZp434P113.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 23-Ju1-1999 #sequence_revision 23-Ju1-1999 #text_change 09-Ju1-2004 C;Accesion: T12529 R;Mambutt. R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. R;Mambutted to the Protein Sequence Database, June 1999 A;Reference number: Z17524 A;Accession: T12529 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1133 <wam> A;Residues: 1-1133 <wam> A;Cross-references: UNIPROT:Q9UG37; EMBL:AL080145 A;Cross-references: UNIPROT:Q9ud37; Colone DKFZp434P113 C;Genetics:</wam></wam>
: : : : :	Db 326 ADVGEQPGEVGYSGSPAEAPPSKSPSWPSL	C; pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C; pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C; Accession: C86446 R; Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudres, B.; Huizar, L. Nature 408, 816-820, 2000 A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Maizili, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome lof the plant Arabidopsis. A; Reference number: A66141; MUID:21016719; PMID:11130712 A; Accession: C86446 A; Status: preliminary A; Molecule type: DNA	A;Cross-treferences: 1-979 <sto> A;Cross-treferences: UNIPROT:Q9FVR3; GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:GC;Genetics: C;Genetics: A;Map position: 1 Query Match Best Local Similarity 21.1%; Pred. No. 6.1; Matches 83; Conservative 47; Mismatches 155; Indels 109; Gaps 19;</sto>	Qy 4 PQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLG 51

, encodin

868 214

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A;Molecule type: mRNA
A;Residues: 1-397 <SCR1>
A;Cross-references: UNIPROT:Q06770; EMBL:X70533; NID:g298114; PIDN:CAA49934.1; PID:g2981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corticosteroid-binding globulin precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C.Accession: 833415, 843740
R.Scrocchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L.
Endocrinology 132, 903-909, 1993
A.Fitle: Spatial and temporal distribution of corticosteroid-binding globulin and its 18, Reference number: 833415; MUID:93145908; PMID:7916682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                    44 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVABANRSQVK 103
                                                                                                                                                                                                                                                                                                                                                                                                                           104 IHTILSNTHRQASRVVLSFD-FPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAP-L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIEL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---APNDKTKSLIREILLSI 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 FQAALHHD-----GRIVFAYKEIPMSVPEISSSQH-----PVKTGLSDAFMILNPSPDV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 TGLEMNMGNVMFLLQNLKLKDSFLADTKHYYESEALTIPSKD----WTKAGEQINNHVK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F:1-22/Domain: signal sequence #status predicted <SIG>F:23-397/Product: corticosteroid-binding globulin #status experimental <MAT>F:89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 NKTQGKIEHVVSDLDSSATLILINYIFLKGIWKLPFSPENTRE-------EDFYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SKVSISKDCIEYY---LSSINILNEFFITYGDSI-----SQISAPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 MANFNPGYSDNSTVVYFD-----NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 MLTATQYVAPLMANFNPGYSDNSTVV-----YFDNGTVFVVQWDHVYLQGWEDKGSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAE----A
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                                                                                                                                                                                                             DB 2; Length 1502;
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                                                                                                                                                                                                                                                               41; Mismatches 106; Indels
                     F;231-247/Domain: transmembrane #status predicted <TM1>
F;434-450/Domain: transmembrane #status predicted <TM2>
F;764-780/Domain: transmembrane #status predicted <TM3>
F;1311-1327/Domain: transmembrane #status predicted <TM4>
F;1382-1399/Domain: transmembrane #status predicted <TM4>
F;1406-1423/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGFDNQYLGFKDI-ISFVSLDVQKDLVKLDFKDLF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDL 301
                                                                                                                                                                                                                                         Pred. No. 18;
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Pred. No. 3.
                                                                                                                                                                                                           4.4%; Score 98; 22.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: glycoprotein; steroid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.48;
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Best Local Similarity 20.2%;
Matches 53; Conservative
                                                                                                                                                                                                                                      Best_Local Similarity 22.7%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 23-40 <SCR2>
C; Superfamily: Serpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S43740
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A.Residues: 1-1502 <0BW>
A.Cross-references: EMBL:X79489; NID:g496661; PIDN:CAA56029.1; PID:g496702
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             877 AIHKFDKFNMNISGVFHPNGLEVIINTEIWDLRTFHLLHTVPALDQCRVVFNHTGTVMYG 936
                                                                                                                                                                                                                                                                                                                                                                       AFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTC-LOHRSCDACMSSD 300
                                                                                                                                                                                                                                                                                                                                                                                                     ---AQEAEGRMCEDFQDEDH 347
                                                                                                                                                                                                                                                                 -----PMSVPEISSSQ---HPVKTGLSD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBL0725
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 09-Jun-1994 #sequence erevision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S45429; S45820; S45815; S59226
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A;Description: Sequence analysis of a 78,6 kb segment of the left end of Sac A;Reference number: S45387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A;Residues: 1-1502 <OBE>
A;Residues: 1-1502 <OBE>
A;Cross-references: UNIPROT:P38181; EMBL:X79489; NID:g496661; PID:g496702
A;Experimental source: strain S288C
R;Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
Bubmitted to the Protein Sequence Database, August 1994
A;Reference number: 845816
A;Accession: 845820
                                                                                                                                                         145 GDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQG--WE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1502 < DDM>
A; Residues: 1-1502 < DDM>
A; Cross-references: EMBL: 325840; NID: 9536126; PID: 9536127; MIPS: YBL079w
A; Experimental source: strain $288C
R; Contreras, R.; Fiers, W.; Logghe, M.; Molemans, F.
submitted to the Protein Sequence Database, August 1994
A; Reference number: $45802
A; Accession: $45815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1041 DEDDDDTD-----DLDELDTDQLLEAELEEDDN--NENAGEDG-DNDFSP 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSASPDISFSPYDGDLTTISSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSP 398
                                                                                                        68;
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A;Status: nucleic acid sequence not shown; translation not shown
                                                    DB 2; Length 1133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1262-1502 <CON>
A; Residues: 1262-1502 <CON>
A; Cross-references: EMBL.52840; MIPS:YBL079w
A; Cross-rimental source: strain S288C
R; Obermaler, B; Gassenhuber, J.; Piravandi, E.; Domdey, H.
Yeast 11, 1103-1112, 1995
A; Title: Sequence analysis of a 78.6 kb segment of the left end A; Reference number: S59184; MUID:96076635; PMID:7502586
                                                                                                        Indels
                                                    4.5%; Score 99; DB 2; Le 23.0%; Pred. No. 10; ive 37; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTFNCSWCHVLQRCSSGFDRYRQEWMDYGC---
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A;Cross-references: SGD:S0000175; MIPS:YBL079w
A;Map position: 2L
                                                                                                                                                                                                                                                               198 ----DKGSFTFQAALHHDGRIVFAYKEI-
                                                                                                        Conservative
                                                                          Similarity
A; Note: DKFZp434P113.1
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                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                       242
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                                                    Query Match
Best Local
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                                                                                                  Matches
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VVAALNRDTIDRWGKLMIP-ROWN	115 ASRVVLSPDFPFYGHPLRQITIATGGFIFWGDVIHRMLTATQYVAPLMAN
328	DD 46 SSEIKLSVYFIFFKSFYKKIVIVNNNGVISFNSLVSQFIFEAFFLALGKAFVAFFCGUVAN 105 QY 165FNPGXŞDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSF 202
OF THE PERSON OF	Db 106 GIRGEIYYRESTNPELLGESSKDIRKYFKDMASFSASWVFIVTWEEVQFYGGSSTT 161
119703 hypothetical protein C34C12.2 - Caenorhabditis elegans	
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004 C;Accession: T19703	
KiACERanw, as a submitted to the EMBL Data Library, December 1994 A;Reference number: 219166	Db 220 FSIPGSRTPDIVNIEGTTNVNIPGRMAFKIDGREIDPANLS 260
Accession: 119703 Status: preliminary; translated from GB/EMBL/DDBJ Molecule tvoe: DNA	RESULT 12
PIDN:CAA87102.1; GSPDB:GN00021; CESP:C3	NEDD-4 ORF - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Genetics: A;Gene: CESP:C34C12.2 A;Map position: 3 a:Throne: 5/3: 72/3: 126/3: 511/3: 605/3	C;Accession: 183196 R;Kumar, S.; Tomooka, Y.; Noda, M. B;Ochem. Biochye. Res. Commun. 185, 1155-1161, 1992 B:Ochem. Biophye. Ase. Commun. 185, 1155-1161, 1992
.5; DB 2; Length 679;	
Matches 65; Conservative 31; Mismatches 105; Indels 65; Gaps 12;	A;Molecule type: mRNA A;Residues: 1-708 <res></res>
OY 34 SPGHVSEDKTOZODLGGGTLAMDTLPDNRTRVVEDNHSYYVSELYGPSEDHYDD 93 DD 372 SPGPPGRTOISDQLNTGEVRYVVNSGKPFNFSSESNSRNLKLI 414	
OY 94 VAEANRSOVKIHTILSNTHRQASRVVLSFDFFYGHPLRQITIATGGFIFM 144 :	C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui F;40-77/Domain: WW repeat homology <wml>> F;186-233/Domain: WW repeat homology <wwl>> F;251-288/Domain: WW repeat homology <wwl>></wwl></wwl></wml>
ANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDK 199	F;347-682/Domain: ubiquitin-protein ligase homology <ubi></ubi>
467 PDISSTPYKSHVVVESDEMNSSSSTIGGFESEKKDNGALGSQKS	Query Match Query Match Best Local Similarity 19.3%; Pred. No. 11. Matches 91; Conservative 50; Mismatches 150; Indels 180; Gaps 24;
Qy 200 GSFTFQAALAHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRS 259 Db 511 PMPDIATALHNIFDSKEVQSSSSTTGSSAPPENSKKSDHFDMPDISSTLYRS 562	OY 5 OPCAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPD
Oy 260 IPEYHRIELDPSKVTSMSAVEFTPLP 285 Db 563 RVEPISSSSGGTSTSAPRYVPKP 586	43RTQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSR-LYGPSEP
RESULT 11	Qy 86 HSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGF 141
grant tectorin - chicken C.Species: Gallus callus (chicken)	Db 138 HIDVQTHLAEEFNTRLAVCGNPATSQPVTSSNH 170
C.Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004 C.Accession: T30243 R.Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.	QY 142 IFWGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYL 193 : : : : : : : : :
<pre>sar. Res. 130, 62-74, 1999 Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis. Reference number: Z20783; MUID:99251817; PMID:10320099 Accession: T30243</pre>	Qy 194 QGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEI 228
Status: preliminary; translated from GB/EMBL/DDBJ	229
A,ROBIQUES: 1-2120 CCUD. A,ACTOSE-references: UNIPROT:09YH85; EMBL.AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAd A,Note: non-collagenous protein only expressed in the inner ear	282 PRLCHVAITGPAVFYSRDYRKKEFFRKKLKKQTDIPNK
Query Match 4.3%; Score 95.5; DB 2; Length 2120; Best Local Similarity 24.4%; Pred. No. 46; Matches 54; Conservative 28; Mismatches 72; Indels 67; Gaps 13;	Cy 28B LORESCDACMSSDLTFNCSWCHYLORGSGFDRYROGWHDYGCAGEAGGRWEDFGDF 345 Db 321 FEMKLRRANILEDSYRR-IMGVKRADLLKARLMIEFDGEKG 360

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24;

Gaps

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C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui P;54-167/Domain: protein kinase C C2 region homology «KC2» P;246-283/Domain: WW repeat homology «WW1» P;402-439/Domain: WW repeat homology «WW2» P;459-496/Domain: WW repeat homology «WW3» P;555-881/Domain: www.repeat homology «WW3» P;555-881/Domain: ubiquitin-protein ligase homology «UBI»
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A; Cross-references: UNIPROT: Q60673; EMBL: U11812; NID: 9563737; PIDN: AAA52102.1; PID: 95637
A; Experimental source: brain
B; Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A; Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
A; Reference number: $40280
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A; Residues: 801-837,839-852,'T',854-907 <HEN>
A; Cross-references: EMBL: Z23060; NID: 9438157; PIDN: CAA80595.1; PID: 9438158
A; Magistralli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
Biochem. Biophys. Res. Commun. 217, 154-161, 1995
A; Title: Expression of PTP35, the murine homologue of the PTP2 se-related sequences 1A-2
A; Reference number: 148721; MUID: 96095652; PMID: 8526904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 SQHPVKTGLSDAFMILNPSPDVPESR-RRSIFEYHRIELDPSKVTSMSAVEFTPLFTCLQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 MK-------LRRANILEDSYRR-IMGVKRADFLKARLWIEFDGEKGLD 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | : | : | CLOAHGAFITRRQISEDVDG-----PDNHESPENWEIVREDENTIYSGQAVQSPPSG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 GSSQTCIFEEQPTLPVLLPTSSGLPPGWEEKQDDRGRSYYVDHNSK-TTTWSKPTMQDDP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 HRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDE---D 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 DVIHRMLTATQYVAPLM----ANFNPGY----SDNSTVVYFDNGTVFVVQWDHVYLQ--- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type N precursor - mous N;Alternate names: protein-tyrosine-phosphatase IA-2 C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: JC2349; S40291; I48721 R;Lu, J: Notkins, A.L.; Lan, M.S. Biochem. Blophys. Res. Commun. 204, 930-936, 1994 A;Title: Isolation, sequence and expression of a novel mouse brain cDNA, mI? A;Reference number: JC2349; MUID:95071416; PMID:7980563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 --PGHVSEPDRTQLSQDLGGGTLAMDTLPDNRTR-----VVEDNHSYYVSR-LYGPSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPDAATHLOHPPEPSPLPPGWEERQDVLGRTYYVNHESRTTOWKRPSPEDDLTDDENGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 HDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDT-KLNPYAG 388
                                                                                                                                                                                                                                                                                                                                                              Indels 175;
                                                                                                                                                                                                                                                                                      Length 887;
                                                                                                                                                                                                                                                                                                                                                           54; Mismatches 151;
                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                      4.2%; Score 93.5; 3.9.1%; Pred. No. 20;
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Best Local Similarity 19.18
Matches 90; Conservative
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A;Residues: 1-887 <STA>
A;Grestences: UNIPROT:Q62940; EMBL:U50842; NID:g1293646; PIDN:AAB48949.1; PID:g129
C;Genetics:
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                                                                                                                                                                                                                                        neprilysin (EC 3.4.24.11) II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: JC7265
R;Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A;Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and A;Contents: Brain and testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: JC7265
A,Molecule type: mRNA
A,Residues: 1-774 <TAN>
C,Genetics: A,Genetics: C,Superfamily: neprilysin
C,Superfamily: neprilysin
C,Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 RIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFE-YHRIELDP- 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 SEPLLNVLDM-IGGWPVAMDKW--NET-------MGPKWELERQLAVLNSQFN 224
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-DHDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAG 388
                                                                361 LDYGGVAREWFFLISKEMFNPYYG-----LFEYSATDNYTLQINPNSG 403
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21.3%; Pred. No. 15;
tive 44; Mismatches 123; Indels
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A;Accession: I48721
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: "MFPCARGERSSERGR',1-165, 'GDGAGA',170-362,'L',364-614,'V',616-674,'T',676-858
A;Cross-references: EMBL:X74438; NID:g1089901; PIDN:CAA52453.1; PID:g1089902
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase, receptor type N #status predicted c;N-137/Domain: stynal sequence #status predicted cs1G>
F;38-979/Domain: extracellular #status predicted cxxr>
F;577-598/Domain: intracellular #status predicted cxxr>
F;577-598/Domain: protein-tyrosine-phosphatase homology cPTP2>
F;566-524/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;909/Active site: Cyb (phosphotate (Arg) #status predicted
F;915/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 RSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNC--SWC----- 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.2%; Score 93.5; DB 1; Length 979; Best Local Similarity 23.0%; Pred. No. 23; Matches 38; Conservative 23; Mismatches 55; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 TSFSPYDG-----DLTTTSSSLFIDSLTTEDDTKLNPYAGGDG 391
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Search completed: January 28, 2005, 22:12:44 Job time : 30.3934 secs

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Matches 410
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0982v9 drosophila
018500 caenorhabdi
0701f6 anopheles g
0702j8 anopheles g
0702j8 anopheles g
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Million cell updates/sec
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                                                                                                                                                  US-09-918-715-230_COPY_18_427
2218
1 ALSPQPGAGHDEGPGSGWAA.......GLQNNLSPKTKGTPVHLGTI 410
                                                                                                 time 139.695 Seconds
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              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                              January 28, 2005, 21:55:21; Search (without 1688.701
                                                                                                                                                                                                                                                                                 Fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Q9HCT9
Q81UK5
Q91ZV7
Q9CWV5
Q9CWV5
Q9EBM20
Q6BM20
Q6BM20
Q6CW71
Q9CW71
Q9CW71
Q91ZV6
Q9CET5
Q9GET5
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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09gz22 homo sapien
06gz22 homo sapien
06gz4 brachydanio
Aah5966 brachydan
09f1t3 streptococc
09fb48 corynebacte
06py3 schistosoma
Aas66254 schistoso
068868 synechococc
Q9h3q7 homo sapien
Q9ukw9 homo sapien
P4308 chizobium s
Q6urrs xenopus la
Aaq62573 xenopus la
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MEDLINE-21443268; PubMed=11559528;
MEDLINE-21443268; PubMed=11559528;
Kinzler E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
05-JUL-2004 (TrEMBLrel. 17, Last annotation update)
Tumor endothelial marker 7 precursor (Tumor endothelial marker 3
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Vogelstein B.,
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tumor endothelial marker 3.
C545A16619EEDBED CRC64;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20407466; PubMed=10947988;
St Croix B., Rago C., Velculescu V., Traverso G.,
Montgomery E., Lal A., Riggins G.J., Lengauer C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2218; DB 2;
100.0%; Pred. No. 4.2e-174;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Gence expressed in human tumor endothelium.";
Science 289:1197-1202(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                          500 AA.
                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
  09H3Q7
9QUKW9
PPCK RHISN
06URR
AAQ62573
09H195
0GFB14
Q6PB14
Q6PB14
Q9PB13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             humans.";
Cancer Res. 61:6649-6655(2001).
BMBL, AP279144, AAG00869.2; -.
BMBL, AP378753; AAL11990.1; -.
GO; GO:0001525; P:angiogenesis; NAS.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
Ffam; PF01437; PS1; 1.
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AAS68254
068868
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21443268; PubMed-11559528;
Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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                                                                                                                        99.9%; Score 2215; DB 2; Length 500; 99.8%; Pred. No. 7.5e-174; tive 1; Mismatches 0; Indels (
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500 tumor endothelial marker 7.
55693 MW; 14FE25512A319DAF CRC64;
InterPro, IPR002165; Plexin_repeat.
Pfam; PF01437; PS1; 1.
SMART; SM00423; PS1; 1.
SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0912V7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name-Plxdcl; Synonyms=Tem7;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 AA
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MGD; MGI:1919574; Plxdc1.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003165; Plexin-like.
Pfam; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
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                                                                                                                                                                                Matches 409; Conservative
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SEQUENCE FROM N.A.
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CHAIN
SEQUENCE
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X Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A HOPKINE R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Roank S.A., McKeran P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Fahley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Radriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

R Gones S.J., Marra M.A.;

R "Generation and initial analysis of more than 15,000 full-length human
                                78 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
                                                                                                        SFDFFFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                                                        138 SFDFPFYGHDLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 197
                                                                                                                                                                                                                                        GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIFWSVPEISSSQHPVKTGLS 257
                                                                                                                                                                                                                                                                                                                 DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                                                                                                            DAFMILNDSPDVPESRRRSIFBYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 317
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     PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                                                                                                                                                           GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPRISSSQHPVKTGLS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI 410
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                  GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS 240
                                                                                                                                                                                                                                                                     DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL
                                                     1 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                            Gaps
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-21085660; PubMed-11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
                                                                                                                                                                                                                                                                                                                                                                                GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI 410
                                                                                                                                                                                                                                                                                                                                                                                                          427
                          1;
Length 500;
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81.1%; Score 1799.5; DB 2
80.7%; Pred. No. 1.3e-139;
ive 39; Mismatches 39;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=99279253; PubMed=10349636;
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Mammalia; Eutheria; Rodentia;
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                            Conservative
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Query Match
Best Local Similarity
Matches 331; Conserv
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STRAIN=C57BL/6J;
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
M. Hanagaki T., Hara Y., Kono M., Izawa M., Kasukawa T., Kato H.,
A. Rawai J., Kojima Y., Konon H., Kouda M., Koya S., Kurihara C.,
M. Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogbe Y., Suzuki H., Tagami M., Tagawa A., Takahahi F., Tanaka T.,
Muramatsu M., Hayashizaki Y.;
Muramatsu M., Hayashizaki Y.;
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; MC010361; BAB26881.1; -.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0014872; F:receptor activity; IEA.
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w genes.";
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              Itoh
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     Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Perparalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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500 AA; 55635 MW; 802D6865F8CA18BD CRC64;
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Local Similarity 80.5%; Pred. No. 4.2e-139;
Les 330; Conservative 39; Mismatches 40;
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InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                  STRAIN=C57BL/6J;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20499374; PubMed=11042159;
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Pfam; PF01437; PSI;
SMART: SM00423; PSI
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LTFNCSWCHVLQRCSSGFDRYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASPDSSFSPFN 378
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MEDLINE=20499374; PubMed=11042185;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Cerebellum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 660, 770 full-length cDNAs.";
Nature 420:563-573 (2002).
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Natsuira I., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
                                               410
                                                                     GD-STTSSSLFIDSLTTEDDTKLNPYARGDGLPDHSSPKSKGPPVHLGTI
                                             GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CS7BL/6J; TISSUE-Cerebellum;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE-2108566; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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319 DTCVSSNLTFNCSWCHVLQRCSSGFDRYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASFD 378
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Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kathara K., Kojima Y., Kondo B., Konno H., Kouda M., Koya S. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towa T., Yasunishi A., Muramatsu M., Hayashizaki Y.; EMBL, AK036144; BAC29318.1;
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
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C2D50B44561C3415 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; P:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003165; Plexin_like.
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                                                                                                           HPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQW
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Genome Res. 13:2265-2270(2003).
EMBL; AY358486; AAQ88850.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Last annotation update)
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InterPro; IPR002165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
SMART; SMO422; PSI; 1.
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HVLQRSLNNQD 329
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Best Local Similarity
Matches 205; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVXTGLSDAFMILNP 258
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                                                                                                                                                                                                                                                                                  PGSGWAAKGTVRGWNRRARESPGH-----VSEPDRTQLSQDLGGGTLAMDTLPDNRTRVV 68
                                                                                                                                                                                                                                                                                                                                                                     EDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSPDFPYG
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BAC87025;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2014 (TrEMBLrel. 27, Last annotation update)
CDNA RL445632 fis, clone CHONS2001834, highly similar to Homo sapiens tumor endothelial marker 7 (TEM7).
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                                                                                                                                                                                                                                                                                                                             PKEGFONAGP---WETGSQSDSSHKPQGASSAPPRTWPHQGAQGNE------
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 PKEGFQNAGP---WETGSQSDSSHKPQGASSAPPRTWPHQGAQGNE-----
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Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AK127539; BAC87025.1; -
InterPro; IPR001165; Plexin_repeat.

Pfan; PF01437; PSI; 1.

SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK127539; BAC87025.1;
SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;
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82.6%; Pred. No. 8.8e-101;
iive 4; Mismatches 28;
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DACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPD 353
                                                             394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQH 233
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Bifort to Identify Novel Human Secreted and Transmembrane Proteins:
Bioinformatics Assessment ";
Genome Res. 13:2265-2270(2003).
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Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
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Last annotation update)
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Best Local Similarity
Matches 205; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      GTI 410
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                                                                                                                                                                                                                                                                                   T--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ-NNLSPKTKGTPVHL 407
                                                                                                                                                                                                                                                                                                                          QASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQH 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVRYFDNGTALVVQWDHVHLQDNYNLGSFTEQATLLMDGRIIFGYKEIPVLVTQISSTNH 274
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                                                                                                                                                           294 DACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPD 353
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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31 529 tumor endothelial marker 7-related.
529 AA; 59583 MW; D44A0975DF894840 CRC64;
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MEDIJNE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 529;
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Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation u
Tumor endothelial marker 7-related precursor.
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GO: GO: 0016020; C: membrane; IEA.
GO: GO: 00004972; F: receptor activity; IEA.
GO: GO: 0007275; P: development; IEA.
InterPro: IPR003659; Plexin_like.
InterPro: IPR003659; Plexin_repeat.
Ffam; PF01437; FSI; 1.
SWART; SM00423; PSI; 1.
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EMBL; AF378757; AAL11994.1; -.
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XI STRAIN-WRI; TISGUE-Mammary tumor. WAP-Tag model. 5 months old;

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Zeeberg B.A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B.B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

XI Standeron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XI Standeron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XI Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XI Standeron B., Wetreman N., Madan A.M., Gay L.J., Hulyk S.W.,

XI Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XI Halton B.K., Warny D.M., Gaergren E.J., Lu X., Gibbs R.A.,

XI Halton M.Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XI Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XI Nortey W., Touchman J.W., Green E.D., Dickson M.C.,

XI Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XI Generation and initial analysis of more than 15,000 full-length human
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51.3%; Pred. No. 2.7e-77;
ive 67; Mismatches 112; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=NWRI; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stransberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057881; AAH57881.1;
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FREM: PF01437; PSI; 1.
SMART; SW00423; PSI; 1.
SEOUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
                                                                                                                                                                                                                 (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                  530 AA
                                                                                                                                                                                          Created)
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Tumor endothelial marker 7-related,
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Best Local Similarity 51.39
Marches 203; Conservative
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                                        457
  GTI 410
                                        GLI
                                                                                                                                                                                                                                                                                Name=Plxdc2;
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408
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                                                                                              RESULT 11

Q6 PETS

ID Q6 PETS

AC G6 PETT

AC G6 PETT

AC G6 PETT

DT G5-JU

DT G5-JU

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375
                                        363 RÓDWVDSGCPEEVQSKEKMCEKTEPGETSQTTTTSHTTTMQFRVLTTTRRAVTSQMPTSL 422
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN tull-length enriched library,
clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C55EL/6J; IISSUE=Lung; MEDLINE=20499374; PubMed=11042159; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; pubtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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EYHRIBLDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRY
                                                                                                                                                     RQEWMDYGCAQEAEG--RMCEDFQDEDHDSASPDTSFSPYDGDLTTTS----SSLFIDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci P.,
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SEQUENCE FROM N.A.
STRAIN=C7PL/61; TISSUE=Lung;
SETRAIN=C7PL/61; TISSUE=Lung;
SETRAIN=C7PL/61; TISSUE=Lung;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSOrtium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                        PTEDDTKIALHLKDSGASTDDSAAEKKGGTLHAGLI 458
                                                                                                                                                                                                                                                                                                           376 TTEDDIKLNPYAGGDGLQ-NNLSPKTKGTPVHLGTI
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Lung;
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Nature 420:563-573(2002).
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     NCBI_TaxID=10090;
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                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adadai J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akahira S., Rukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kach H.,

Imorani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kach H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

M Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

M Kawai J., Nolido T., Owa C., Saito R., Sakai K.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Salio R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Zalio R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Salio R., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Sakinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Rogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Rojaha Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Bulli, Akoole464; Bab234311; -.

Co. Go.:0004640; Bab234311; -.

Bulli, Akoole40; Ramazare; IEA.

GO; GO::0004872; F:receptor activity; IEA.

Roja Go::0004872; F:receptor activity; IEA.

Roja Go::0004872; F:receptor activity; IEA.

Rossell Rolling M., PLC. Nuclease.

Rick Perco; IPRO08565; Plexeral Like.

Roccord Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Rolling M., Roll
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (Mouse)
102-MAR musculus (Mouse)
102-MAR musculus (Mouse)
103-MAR musculus (Mouse)
103-MAR mania; Marianse; Murinas; Mus.
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51.3%; Pred. No. 2.7e-77;
ive 67; Mismatches 112; Indels 14;
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Pfam; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
SEQUENCE 530 AA; 59616 MW; PB956C020735E36D CRC64;
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Genome Res. 10:1757-1771(2000)
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Best Local Similarity 51.3%;
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GN Name=
OC BURB 10
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        1 30 Potential.
31 530 tumor endothelial marker 7-related.
530 AA; 59625 MW; FF8315020735836D CRC64;
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 47.1%; Score 1044; DB 2; Length 530; Local Similarity 51.3%; Pred. No. 2.7e-77; les 203; Conservative 67; Mismatches 112; Indels 14
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SEQUENCE FROM N.A.
STRAIN=NMRI; TISSUE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH57881;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Tumor endothelial marker 7-related.
Mus musculus (Mouse).
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SMART; SM00423; PSI; 1.
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Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleron M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., MRIchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., G., Mones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                     Gaps
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Kenopus laevis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus.

NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                              530;
                                                                                                                                                                                                                                                                                                                                    67; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                              47.1%; Score 1044; DB 2; Length 51.3%; Pred. No. 2.7e-77;
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRANIB-NMI!, TISSUE-Mammary tumor;
Stransberg R.
Stransberg (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                          EMBL; BC057881; AAH57881.1; -. SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
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                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.P., Jozdan H., Moore T., Max S. I., Wang J., Haich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Socres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan R.J., Malke J.A., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Radigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEW
                    Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.6%; Score 1034.5; DB 2; Length 513; 51.3%; Pred. No. 1.6e-76; Live 69; Mismatches 106; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC077242; AAH77242.1; -.
Hypothetical protein.
SEQUENCE 513 AA; 57622 MW; 301EA53F2905A4ÉD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      larity 51.3%;
Conservative 6
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les 200; Conserv
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                      PubMed=12477932;
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                                                                                                                                       initiative.
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Search completed: January 28, 2005, 22:11:23 Job time : 141.695 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:21; Search time 22.1468 Seconds

(without alignments)

1688.701 Million cell updates/sec
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1688.701 Million cell updates/e
Title: US-09-918-715-230_COPY_280_344
Perfect score: 370
Sequence: 1 YHRIELDPSKVTSMSAVEFT........CHVLQRCSSGFDRYRQEWMD 65

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

aximum DB seq length: zooooooo

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_02:* 1: uniprot_sprot:* 2: uniprot_trembl:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Q8iuk5 homo sapien	Q9hct9 homo sapien	O9cwv5 mus musculu	Q91zv7 mus musculu	Q8bm20 mus musculu	Q6zsc8 homo sapien	Bac87025 homo sapi	Q6pet5 mus musculu	Q9dc11 mus musculu	Q91zv6 mus musculu	Aah57881 mus muscu	homo	homo	Q96pd9 homo sapien	0 homo	Q6de92 xenopus lae	Q9w2v9 drosophila			Q7q2j8 anopheles g	Q8cjh3 mus musculu	045657 caenorhabdi			Q6dcp0 xenopus lae	Q6ny20 homo sapien	73 hon	Q9uj92 homo sapien	homo		P90641 paramecium
QI	Q8IUKS	Q9HCT9	Q9CWV5	Q912V7	Q8BM20	Q6ZSC8	BAC87025	Q6PETS	Q9DC11	Q912V6	AAH57881	Q96E59	Q6UX71	60496D	AAQ88850	Q6DE92	Q9W2V9	Q18500	060486	Q7Q2J8	О 8СЛН3	045657	CAB05755	Q9UJ93	Q6DCP0	Q6NY20	AAH66773	. Q9UJ92	CAIN6D	043157	P90641
DB	2	7	7	~	N	7	N	~	N	~	~	~	Ŋ	~	N	~	~	N	N	~	~	~	~	~	~	~	~	~	~	N	C3
Length	500	200	200	200	507	351	351	530	530	530	530	480	529	529	529	513	625	498	1568	384	2119	1764	1764	729	835	1832	1832	1952	2135	2143	206
% Query Match	100.0	100.0	87.8	87.8	87.8	77.6	77.6	71.4	71.4	71.4	71.4	71.1	71.1	71.1	71.1	67.8	46.5	37.0	27.3	27.2	24.5	22.7	22.7	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.3
Score	370	370	325	325	325	287	287	264	264	264	264	263	263	263	263	251	172	137	101	100.5	90.5	84	84	83.5	83.5	83.5	83.5	83.5	83.5	83.5	82.5
Result No.	1	8	m	4	Z.	9	. 7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q8c3x9 mus musculu Q8cgwl mus musculu Q9gzc2 mus musculu Q86c23 schistosoma Q6pyv2 schistosoma Aas68255 schistosome P51805 homo sapien Q769i5 bos taurus Bad05055 bos tauru O7501 homo sapien P70208 mus musculu Q91823 xenopus lae Q6ybw0 trichinella
•
Q8C3X9 Q8CGW1 Q9QCC2 Q8GE23 Q6EXY2 AAS68255 PLIX HUMAN Q9IW11 Q76915 BAD05055 P70208 Q91823 Q91823
0000000000000000
749 1205 190 190 343 343 343 1928 11384 11963 1905 676
200.00 200.00 200.00 200.00 200.00 200.00 200.00 200.00 200.00
82 82 81 81 81 80 5 80 80 80 77 76 5 76

ALIGNMENTS

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**X TASUBE-188118;

**X MEDLINE=2238825; PubMed=12477932;

**A KEDLINE=2238825; PubMed=12477932;

**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Haie F.,

**A Brothenko L., Marusha R., Farmer A.A., Rubin G.M., Hong L.,

**A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Bosak S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Nilalon M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

**Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

**A Rodiguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**A Tones S.J., Marra M.A.;

**Jones S.J., Marra M.A.;

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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036059; AAH36059.1; -
Genew; HGNC:20945; PLXCDC;
GO; GO:0016020; C:membranc; IEA.
GO; GO:001607275; P:teceptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR003659; Plexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;
                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Plexin domain containing 1,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                       500 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 370;
                                                       PRT;
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                                                       PRELIMINARY;
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SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                     rissum=Testis;
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                                                                                                                                                                                                                   Name=PLXDC1;
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RESULT 1
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                                                                                                                       280 YHIELDPSKVISMSAVEFIPLPTCLQHRSCDACMSSDLIFNCSWCHVLQRCSSGFDRYR 339
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                                                                                      1 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR
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                             Gaps
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Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-007-2001 (TrEMBLrel. 18, Last sequence update)
05-001-2004 (TrEMBLrel. 27, Last annotation update)
15-001-2004 (TrEMBLrel. 27, Last annotation update)
15-001-2004 (TrEMBLrel. 7) precursor (Numor endothelial marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Vogelstein
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
tumor endothelial marker 3.
C545A16619EEDBED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
St Croix B., Vogelstein B., Kinzler K.W.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20407466; PubMed=10947988;
St Croix B., Rago C., Velculescu V., Traverso G.,
Montgomery E., Lal A., Riggins G.J., Lengauer C.,
  Pred. No. 3.3e-35;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genes expressed in human tumor endothelium.";
                                                                                                                                                                                                                                                                                                                                                                                                              500 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF279144; AAG00869.2; -
EMBL, AF379753; AAL11990.1; -
GO; GO:0001525; P:angiogenesis; NAS.
InterPro; IPR003165; Plexin-like.
InterPro; IPR003165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer Res. 61:6649-6655(2001).
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100.08;
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                             65, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
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QEWMD 344
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RESULT Q9CWV5

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the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamanoto R., Mateuuna S., Hazama M., Nishine T., Kashiwagi K., Yamanoto R., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Nishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Rishikawa T., Sawa K., Tanaka T., Mateuura S., Kawai J., Rishikawa T., Sawa K., Tanaka T., Mateuura S., Kawai J., Rishikawa T., Sawa M., Inoue Y., Kira A., Hayashizaki Y.; Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika I., Mateuura S., Kawai J., Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Rishika Ri
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                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
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RIKEN PANYOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
Q9CWV5 PRELIMINARY; PRT; 500 AA.
Q9CWV5;
Q01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=20499374; PubMed=11042159;
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Nature 420:563-573(2002).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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MEDLINE=21443266; PubMed=11559528;
MEDLINE=21443266; Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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84.4%; Pred. No. 6.8e-30;
ive 7; Mismatches 3; Indels
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MGD; MGI:1919574; Plxdcl.
GO; GO:001620; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000775; P:development; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003165; Plexin-like.
InterPro; IPR003165; Plexin-like.
InterPro; IPR01516; Plexin_repeat.
Pfam; PF01477; PSI; 1.
SMART; SM00423; PSI; 1.
SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;
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GO; GO:0004872; F:receptor activity; IBA...

GO; GO:0007275; P:development; IEA...

InterPro; IPR007110; Ig-like...

InterPro; IPR003165; Plexin-like...

Pfam; PF01437; PSI: 1.
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EMBL; AF378760; AAL11997.1; -.
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ESQUENCE FROM N.A.

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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Cerebellum;

STRAIN=C57BL/6J; TISSUE=Cerebellum;

MEDLINE=20530913; PubMed=11076861;

A Shibatea K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Anbibatea K., Inch M., Alzawa K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishlii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishlii Y., Nakamura S., Izawa M., Ohara E., Kashiwagi K., Pujiwake S., Inoue K., Tanaka T., Natsuura S., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Anakaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system=384-format sequencing pipeline with 384 multicapillary sequencer.";
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatun N., Haramoto K., Hiraoka T., Hirozane T.,

Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Saito K., Saitoh H., Sakai C., Sakai K., Sakaume N., Sanoh

Sasto S., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate cerebellum CDNA, RIKEN full-length
enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER
                                                                                                                                                                                                                                                                                                                                             Name-Pĭxdc1;
Nam musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
Hitph-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
507 AA.
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STRAIN-C57BL/6J; TISSUE-Cerebellum;
The FANTOM Consortium,
PRT;
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
         PRELIMINARY;
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         Q8BM20
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sapiens (Human)
                                                                    NCBI_TaxID=9606;
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A Gehlma A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
A Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
A CIGNKI T., Sato H., Wakamateu A., Imabayashi H.,
CUSUKI T., Sato H., Wakamateu A., Imabayashi H.,
A Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
A Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanchori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (Jul.-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AKL27539; BAC87025.1; -.
InterPro; IPR002165; Plexin_repeat.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2002 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ45632 fis, clone CHONS2001834, highly similar to Homo sapiens tumor endothelial marker 7 (TEM7).
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Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; AK036144; BAC29318.1; -.
R MGD; MGI:1919574; Plxdcl.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0004872; F:receptor activity; IEA.
R GO; GO:0007275; P:development; IEA.
R InterPro; IPR003659; Plexin-like.
R InterPro; IPR003165; Plexin-like.
R InterPro; IPR003165; Plexin-like.
R InterPro; SM00423; PSI; 1.
R Pfam; PF01437; PSI; 1.
R Pfam; PF01437; PSI; 1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FL745632.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.6%; Score 287; DB 2;
91.2%; Pred. No. 1.5e-25;
iive 1; Mismatches 4;
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84.4%; Pred. No. 6.9e-30;
ive 7; Mismatches 3
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Best Local Similarity 84.1.
Best Local 54; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=NMRI; TISSUE=Nammary tumor. WAP-Tag model. 5 months old;

Kausner R.D., Felingold E.A., Grouse L.H., Derge J.G.,

Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.R., Schuler G.D.,

Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleron M., Soares M.B., Bonaldo M.F., Caarvant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roark S.A., McEwan P.-J., McKernan R.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Rahebley J., Helton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rad Marra M.A.,

Togeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRSLNNQD 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YHRIBLDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFD 57
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                                                                                                                                                                                                       Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Ostsuki T., Sato H., Wakamatsu A., Imbaayashi H., Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nahikawa T., Kimura K., Yamashita H., Matsuo K., Nahikawa K., Kanchori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project.", Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.6%; Score 287; DB 2; Length 35
91.2%; Pred. No. 1.5e-25;
tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK127539; BAC87025.1; -.
SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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STRANT-CSTBL/GJ; TISSUE-Lung;
STRANT-CSTBL/GJ; TISSUE-Lung;
The FANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
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SEQUENCE FROM N.A.
STRAIN=C57BL/64; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                           1 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR
                                                                                                                                                                                                             Gaps
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STRAIN=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Tamamoto R., Matsuncto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=21085660. PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                            Length 530;
                                                                                                                                         71.4%; Score 264; DB 2; Length 53 67.7%; Pred. No. 1.2e-22; ive 9; Mismatches 12; Indels
Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
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MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Yi.
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                          44; Conservative
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                                                                                                                                                                       Similarity
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364 QDWVD 368
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Best Local
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STRAIN-C57BL/63; TISSUE-Lung;
Adachi J. Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Pukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Cazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; P:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR008947; PIC_Nuclease.
InterPro; IPR003659; Plexin_like.
Pfam; PF01437; PSI; 1.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:devalopment; IEA.
InterPro; IPR003659; Plexin_like.
InterPro; IPR00265; Plexin_repeat.
Pfam; PF01437; PSI; 1.
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Cancer Res. 61:6649-6655(2001).
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Best Local Similarity 67.79
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364 QDWVD 368
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QDWVD 319
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Q6UX71;
                                                                    096E59
                                        RESULT 12
Q96E59
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=NMRI; TISSUE=Mammary tumor;

MEDINE=2238825; PubMed=1247932;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakebley W., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                       tumor endothelial marker 7-related. FF8315020735E36D CRC64;
                                                                                                              ö
                                                                                 Length 530;
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                                                                               71.4%; Score 264; DB 2; Length 53 67.7%; Pred. No. 1.2e-22; ive 9; Mismatches 12; Indels
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STRAIN-NWRI; TISSUE-Mammary tumor;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC057881; AAH57881.1; -.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
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                                                                                                                                                                                                                                                                                              530 AA
                            Potential.
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                                       530 ti
59625 MW;
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Matches 44; Conservative
                                                                                                           44; Conservative
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SMART; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                    530 AA;
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                          364 QDWVD 368
                                                                                                                                                                                               61 QEWMD 65
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                                        CHAIN
SEQUENCE
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AAH57881;
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MEDINE-2538825;

XX MEDINE-2538825;

XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold B.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012885; AAH12885.1;
GO; GO:00146020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:007275; P:developent; IEA.
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CE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;
                                Q96E59;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PLXDC2 protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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    480 AA
    PRT;
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InterPro, IPR002165, Plexin_repeat.
Edm, PF01437, PSI; 1.
SMART, SM00423, PSI; 1.
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Best Local Similarity 67.77
Matches 44; Conservative
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PRELIMINARY;
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ARFP2514.
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Best Local S
Matches 44
                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                              Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis I., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Sembagiri S., Simmons L., Singh J., Sainth V., Stinge M., Stingh J., Sainth V., Stingh J., Sainth V., Stingh J., Vadts A., Vandlen R., Wateanabe C., Wandlen R., Wateanabe C., Waisand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; Genome Res. 13:2265-2270 (2003).

EMBL, AY36846; AAQ88850(1, -...

InterPro; IPR003659; Plexin.like.

InterPro; IPR002165; Plexin.repeat.

SMART; SM00423; PSI; 1.

SMART; SM00423; PSI; 1.

SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NGBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cell surface tumor endothelial markers are conserved in mice and
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MEDIJNE-1443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.1%; Score 263; DB 2; Length 52 67.7%; Pred. No. 1.5e-22; ive 9; Mismatches 12; Indels
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor endothelial marker 7-related precursor.
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EMBL, AF378757, AAL11994.1; -.

Genew, HGNC.121013, PLXDC2.

GO GO:0016020; C:membrne; IEA.

GO; GO:0004872; F:receptor activity, IEA.

GO; GO:0007275; P:development; IEA.

InterPro; IPR003165; Plexin_repeat.

Pfam; PF01437; PS1; 1.

SMART; SM00423; PS1; 1.
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309;
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Matches 44; Conservative
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                                                                                                             Homo sapiens (Human).
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                                                                          ORFNames=UNQ2514;
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AC 096PD9
DT 01-DE DT 01-DE DT 01-DE DT 01-DE DT 01-OC DE ENWART
OC MAMMEN OC MAMMEN (1)
RN KR KRD (1)
RN KRD (1)
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                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
30 Potential.
529 tumor endothelial marker 7-related
59583 MW; D44A0975DF894840 CRC64;
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                                                                                                     Length 529;
                                                                                                                                                     12; Indels
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Last annotation update)
                                                                                                  Score 263; DB 2;
Pred. No. 1.5e-22;
9; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 AA.
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                                                                                                  ch 71.1%;
1 Similarity 67.7%;
44; Conservative 9
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
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31 5
529 AA;
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                                                                                                                                                                                                                                                                                                                                                               364 QDWVD 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 QDWVD 368
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                                                                                                                                                                                                                                                                                                             61 QEWMD 65
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Wed Feb

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

Run on:

January 28, 2005, 21:55:58 ; Search time 4.50139 Seconds (without alignments) 1389.370 Million cell updates/sec

US-09-918-715-230_COPY_280_344 370 1 YHRIELDPSKVTSMSAVEFT.......CHVLQRCSSGFDRYRQEWMD 65 score: Seguence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

1		ا عدد عدد			SUMMARIES	
No.	Score	Match	Length	8	ai.	Description
-	137	37.0	476	7	T19786	hypothetical prote
~	101	27.3	1568	N	T09074	semaphorin recepto
٣	84	22.7	1806	~	T23298	Ţ.
4		20.9	1872	N	JC4976	plexin 3 precursor
'n	76.5	20.7	1905	7	151553	Plexin - African c
9	9/	20.5	1884	~	JC4975	plexin 2 precursor
7	75	20.3	1945	~	T13937	plexin A - fruit f
∞,	74	20.0	1894	N	JC4980	plexin 1 precursor
σ	70	18.9	1379	-	S01254	hepatocyte growth
10	69.5	18.8	465	~	D88448	protein C45G9.8 [i
11	69	18.6	444	~1	G84565	probable flavonol
7	68	18.4	1390	-	TVHUME	hepatocyte growth
[3	67.5	18.2	1375	N	T30813	plasminogen relate
4	67.5	18.2	2051	~	T13164	plexin B - fruit f
κi	67	18.1	174	~	G81349	periplasmic nitrat
بو	67	18.1	1375	Н	JC5148	hepatocyte growth
7	65	17.6	1425	~	T30811	hepatocyte growth
8	64.5	17.4	413	7	H75070	sugar-phosphate nu
61	64.5	17.4	1291	~	T21694	hypothetical prote
20	64	17.3	470	~	H84565	probable flavonol
21	63.5	17.2	846	~	A30889	integrin beta chai
22	63	17.0	1404	Н	A48196	protein-tyrosine k
33	62.5	16.9	439	~	833293	testican - human
4	62.5	16.9	491	~	S31784	VPS protein - bovi
Ž.	62.5	16.9	712	~	T27165	hypothetical prote
9	62.5	16.9	774	N	G71308	probable aminopept
7	62.5	16.9	1042	~	T16169	hypothetical prote
<u></u>	61	16.5	210	~	S76973	hypothetical prote
6	61	16.5	3938	7	T42761	Bassoon protein -

Bassoon protein -	hypothetical prote	hypothetical conse	hypothetical prote	hypothetical prote	probable membrane	protein-tyrosine k	protein F3M18.14 [hypothetical prote	probable SET-domai	hypothetical prote	salivary protein 1	probable zinc fing	hypothetical prote	probable sugar-pho	probable C2H2-type
T42730	S70194	E95974	T16642	T33512	S64850	T30200	E86410	T26588	T00834	T23531	808110	B86382	T08345	A71095	A84431
ď	~	7	~	N	7	7	~	~	7	7	7	~	7	0	N
3942	8	245	548	513	543	1621	1819	338	447	555	311	362	397	416	439
ı,	16.2	16.2	16.2	16.1	16.1	16.1	16.1	15.9	15.9	15.9	15.8	15.8	15.8	15.8	15.8
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61 16		9	09	59.5	59.5	59.5	59.5	59	53	59	58.5	58.5	58.5	58.5	58.5

ALIGNMENTS

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lypothetical protein C36E8.3 - Caenorhabditis elegans
                                      C; Species: Caenorhabditis elegans
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J.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T19786 R;Wilkinson, J.; Barlow, K. submitrot to the EMB. Data Library, August 1994 A;Reference number: Z19177

A; Accession: T19786 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA

A;Cross-references: UNIPROT:018500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3 A;Experimental source: clone C36E8 A; Residues: 1-476 <WIL>

C, Genetics:

A; Gene: CESP: C36E8.3

A;Map position: 3 A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2 C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Gapa 8 37.0%; Score 137; DB 2; Length 476; 37.0%; Pred. No. 8.4e-08; tive 11; Mismatches 27; Indels Local Similarity 37.0% nes 27; Conservative Query Match Matches

23 1 YHRIBLDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLT-FNCSWCHVLQR----CSg à

357 EAGLHRRROHWFE 369 54 -SGFDRYRQEWMD 65 . 유 ò

semaphorin receptor VESPR - human

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09074
R;Comeau, M.R.; Johnson, R.; DuBose, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; P
R;Comeau, M.R.; Johnson, R.; DuBose, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; P
A;Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and bi
A;Reference number: 216555; MUID:98246049; PMID:9586637

A; Accession: T09074

A;Status: prediminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1568 <COM>
A;Residues: 1-1568 <COM>
A;Cross-references: UNIPROT:060486; EMBL;AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3
A;Experimental source: tissue type foreskin; cell type fibroblast
C;Genetics:

A; Gene: VESPR

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R;Ohta, K.; Mizutani, A.; Kawakami, A.; Murakami, Y.; Kasuya, Y.; Takagi, S.; Tanaka, H. Neuron 14, 1189-1199, 1995
Neuron 14, 1189-1199, 1995
A;Title: Plexin: a novel neuronal cell surface molecule that mediates cell adhesion via A;Reference number: I51553; MUID:95329274; PMID:7605632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-1884 «KAM»

A; Residues: 1-1884 «KAM»

A; Cross-references: UNIPROT: P70207; DDBJ: DB6949; NID: g1655431; PIDN: BAA13189.1; PID: d101

C; Comment: This protein is a membrane protein with cell adhesion properties.

C; Comment: This protein is a membrane protein with cell adhesion properties.

C; Keywords: duplication; transmembrane protein

F; 1-21/Domain: signal sequence #status predicted «SIG»

F; 501-549/Region: cysteine-rich duplication

F; 794-845/Region: cysteine-rich duplication

F; 794-845/Region: cysteine-rich duplication

F; 723-1250/Domain: transmembrane #status predicted «TWM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T13937
R;Winberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie Cell 95, 903-916, 1998
A;Title: Plexin A is a neuronal semaphorin receptor that controls axon guidance. A;Reference number: Z17621; MUID:99091049; PMID:9875845
A;Accession: T13937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1945 <WIN>
A;Cross-references: UNIPROT:096681; EMBL:AF106932; NID:g4056673; PID:g4056674; PIDN:AADO
                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPROT: Q91823; GB: D38175; NID: g961514; PIDN: BAA07374.1; PID: g961515
C; Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Hirata, T.; Fujisawa,
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C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                    Plaxin - African clawed frog
C,Species: Xenopus laevis (African clawed frog)
C,Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plexin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 DPSKVTSMSAVEFT -- PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: JC4975
R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, Biochem. Biophys. Res. Commun. 226, 396-402, 1996
A; Title: Identification of plexin family molecules in mice. A; Reference number: JC4975; MUID:96400270; PMID:8806646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 76.5; DB 2; 32.7%; Pred. No. 1.8; iive 10; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.5%; Score 76; DB 2
Best Local Similarity 32.1%; Pred. No. 2;
Matches 17; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: JC4975
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.7*
Matches 16; Conservative
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A, Molecule type: mRNA

A, Residues: 1-1872 - KMA

A, Cross-references: UNINPROT: P70208; DDBJ: D86950; NID: 91655433; PIDN: BAA13190.1; PID: d101

C, Comment: This protein is a membrane protein with cell adhesion properties.

C, Comment: This protein is a membrane protein

E, H-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:045657; EMBL:283232; PIDN:CAB05755.1; GSPDB:GN00020; CESP:Kd
A,Experimental source: clone K04B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:K04B12.1
A;Map position: 2
A;Introns: 24/2; 77/3; 294/2; 378/3; 433/3; 478/3; 523/3; 743/1; 794/3; 1049/3; 1414/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plexin 3 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C;Accession: JC4976
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 396-402, 1996
A;Title: Identification of plaxin family molecules in mice.
A;Reference number: JC4975; MUID:96400270; PMID:8806646
A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                            1 YHRIELDPSK-----VTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein K04B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T23298
R;Steward, C
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19723
A;Accession: T23298
A;Accession: T23298
A;Acturus: preliminary; translated from GB/EMBL/DDBJ
A;Reference DNA
A;Residues: 1-1806 <WIL>
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                      10;
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Pred. No. 1.4;
5; Mismatches 18; Indels 1
                                                       27.3%; Score 101; DB 2; Length 1568; 29.7%; Pred. No. 0.0027; ive 15; Mismatches 27; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 22.7%; Score 84; DB 2; Length 1806; 1 Similarity 43.3%; Pred. No. 0.24; 13; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 SEKQVSQLPVETCEQYLSCAACLGSG-DPHCGWCVLQHRC 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLOHRSCDACMSSDLTFNCSWCHVLQRCSS 54
C; Keywords: receptor; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.9%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                         GDCVHSENLENWLD 498
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                 56 FDRYRQE----WMD
                                                                                        Similarity
                                                                                                                         22;
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                                                              Query Match
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A; Note: the authors translated the codon ACG for residue 1261 as Lys

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A; Title: The Met receptor tyrosine kinase transduces motility, proliferation, and morpho A; Reference number: A45453; MUID:93209981; PMID:8384622
                                                                                                                                                                                                                                                                                                           C;Superfamily: hepatocyte growth factor receptor; protein kinase homology C;Superfamily: hepatocyte growth factor receptor; protein; phosphopransferase; F;1-24/Domain: signal sequence #status predicted <81G>
F;25-929/Domain: extracellular #status predicted <80G>
F;25-930/Domain: extracellular #status predicted <80G>
F;36-302/Product: hepatocyte growth factor receptor alpha chain #status predicted <ACH>
F;308-1379/Product: hepatocyte growth factor receptor beta chain #status predicted <8CH>
F;303-954/Domain: transmembrane #status predicted <TMM>
F;955-1379/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A7500; MID1:99069613; PMID:981916
A;Note: see websites genome.wustl.edu.gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:1108/Active site: Lys #status predicted F:1233/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q09280; GB:chr III; PIDN:AAA62551.1; PID:g687873; GSPDB:GN00
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein C45G9.8 [imported] - Caenorhabditis elegans
D.Species: Caenorhabditis elegans
D.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable flavonol 3-O-glucosyltransferase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RIBLDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE
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60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 EFTPLPT----CLOHRSCDACMSSDLTFNCSWCH----VLORCSSG 55
                                                                                                                                                          A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 1;
Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: D88448
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
;Weidner, K.M.; Sachs, M.; Birchmeier, W.
. Cell Biol. 121, 145-154, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.4%;
Matches 14; Conservative
                                                                                                                                                                                                                         A; Residues: 924-935 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-465 <STO>
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                                                                                                                                                                                        A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508
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A,Residues: 1-1894 «KAM»
A,Cross-references: UNIPROT:P70206; DDBJ:D86948; NID:g1665756; PIDN:BAA13188.1; PID:d101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Experimental source: brain
C:Comment: This protein is a membrane protein, and plays a role in reuronal cell contact
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112) met
S;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S01254; JH0115; Ā45453
R;Chan, A.M.L.; King, H.W.S.; Deakin, B.A.; Tempest, P.R.; Hilkens, J.; Kroezen, V.; Edw
A;Title: Characterization of the mouse met proto-oncogene.
A;Reference number: S01254; MUID:88262253; PMID:2838789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plexin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C;Accession: JC4980
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 524-529, 1996
A;Fitle: Identification of a neuronal cell surface molecule, plexin, in mice.
A;Reference number: JC4980
A;Accession: JC4980
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                                                                                                                                                                                                                         Length 1945;
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                                                       A;Map position: 4
C;Function:
A;Description: may function as repellents during axon guidance
C;Keywords: cell adhesion; nerve
                                                                                                                                                                                                                                                                                       11; Indels
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A;Residues: 'I',1200-1254,'R',1256-1260,'T',1262-1268 <WIL>
A;Experimental source: hemopoietic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sence of calcium ions.
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;1-22/Domain: signal sequence #status predicted <SIG>F;2128-1264/Domain: transmembrane #status predicted <TMM>F;1266-1268/Region: hydrophilic
                                                                                                                                                                                                                  Score 75; DB 2; Pred. No. 2.7; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       672 CSTHSSCTRCVSSE--FPCDWCVEAHRCT 698
                                                                                                                                                                                                                                                                                                                                            25 CLOHRSCDACMSSDLTFNCSWCHVLORCS 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: nucleic acid sequence not shown A,Molecule type: mRNA
A;Gene: plexA
A;Cross-references: PlyBase:FBgn0025741
                                                                                                                                                                                                                     20.3%;
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                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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A,Title: Identification of the major autophosphorylation site of the Met/hepatocyte grown A,Reference number: A40179; MUID:92011756; PMID:1655790
A;Contents: annotation; autophosphorylation site
R;Dean, M.; Park, M.; Vande Woude, G.F.
Mol. Cell. Biol. 7, 921-924, 1987
A;Title: Characterization of the rearranged tpr-met oncogene breakpoint.
A;Reference number: 157632; MUID:87144265; PMID:3821733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A map position: 7431-7431

C. Superfamily: hepatocyte growth factor receptor; protein kinase homology
C. Superfamily: hepatocyte growth factor receptor; phosphoprotein; phosphotransferase; |
E. 1.24/Domain: signal sequence #status predicted <185.
F. 1.24/Domain: signal sequence #status predicted <185.
F. 1.24/Domain: signal sequence #status predicted <185.
F. 1.24/Domain: bepatocyte growth factor receptor alpha chain #status predicted <185.
F. 1981-1990 Product: hepatocyte growth factor receptor beta chain #status predicted <185.
F. 1981-1990 Product: hepatocyte growth factor receptor beta chain #status predicted <185.
F. 1981-1992 Region: protein kinase homology <185.
F. 1981-1992 Region: protein kinase ATP-binding motif F. 1992 Region: protein kinase ATP-binding site: carbohydrate (Asn) (covalent) #status F. 1110/Active site: Lys #status experimental F. 1125/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasminogen related growth factor receptor 2 - Fugu rubripes
C;Species: Rugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30813
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, G.
PBES Lett. 443, 370-374, 1999
A;Title: Three receptor genes for plasminogen related growth factors in the genome of the A;Reference number: 220880; MUID:99148833; PMID:10025966
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M15325; NID:g187531; PIDN:AAA59585.1; PID:g187532
C;Comment: The receptor is a dimer of disulfide-bonded 50K alpha and 145K beta chains th.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 400/3; 459/3; 499/3; 556/3; 611/2; 655/3; 701/2; 761/2; 794/3; 870/3; 919/3; C;Superfamily: hepatocyte growth factor receptor; protein Kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.4%; Score 68; DB 1; Length 1390; 30.4%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 EFTPLPT----CLQHRSCDACMSSDLTFNCSWCH----VLQRCSSG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 KVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: T30813
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 67.5; DE ilarity 32.4%; Pred. No. 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDB:120178; OMIM:164860
                                                                                                                                                                                                                                                                                                              A;Scatus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 963-1009 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 30.4 nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1375 <COT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                          A; Accession: I57632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PRGFR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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A; Residues: 'VNETRECOSLALELEKLANNOLKALTEKNKELEIAQDRNIAIQSQ','FTRTKEELEAEKRDLIRTNERLSQELEY
A; Residues: 'VNETRECOSLALELEKLANNOLKALTEKNKELEIAQDRNIAIQSQ','FTRTKEELEAEKRDLIRTNERLSQELEY
A; Cross = references: GB: U08918; NID: 9487741; PIDN: AAB60323.1; PID: 9487742
A; Note: this activated met oncogene is the product of gene rearrangement
R; Dean, M.; Park, M.; Le Beau, M.M.; Robins, T.S.; Diaz, M.O.; Rowley, J.D.; Blair, D.G.
Nature 318, 385-388, 1985
A; Title: The human met oncogene is related to the tyrosine kinase oncogenes.
A; Reference number: A93369; MUID: 86065462; PMID: 4069211
A; Accession: A93369
A; MOlecule type: DNA
A; Residues: 1267-1390 < DEA>
A; Gandanote, GB: M35074; NID: 9187555; PIDN: AAA59590.1; PID: 9386868
A; Cross = references: GB: M35074; NID: 9187555; PIDN: AAA59590.1; PID: 9386868
A; Cross = references: GB: M35074; NID: 9187555; PMID: 8175700
A; Reference number: A53761; MUID: 94230365; PMID: 8175700
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1390 GIO>
A;Cross-references: UNIPROT:P08581; EMBL:X54559
A;Cross-references: UNIPROT:P08581; EMBL:X54559
B;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
A;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
A;Title: Sequence of MET protooncogene cDNA has features characteristic of the tyrosine
A;Reference number: A28303; MUID:87317655; PMID:2819873
                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9ZU71; GB:AE002093; NID:g4218003; PIDN:AAD12211.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Д.
A, Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A, Reference number: A84420; MUID:20083487; PMID:10617197
A, Accession: G84565
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-444 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brookes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatocyte growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) met C;Species: Homo sapiens (man) 30-Sepecies: Homo sapiens (man) C;Date: 31-Mar-1991 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004 C;Accession: A40175; A28303; A33749; A93369; A53761; I57632; A30008; B24569 R;Giordano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
A, Residues: 1-755, 'TWWKEPLNIVSFLFCFAS', 756-1190,'A',1192-1390 <PAR>
A, Residues: 1-755, 'TWWKEPLNIVSFLFCFAS', 756-1190,'A',1192-1390 <PAR>
A, Crose-references: GB:002988; NID:9180558; PIDN:AAA55591.1; PID:9307196
R;Chan, A.M.L.; King, H.W.S.; Tempest, P.R.; Deskin, E.A.; Cooper, C.S.; Oncogene 1, 229-233, 1987
Oncogene 1, 229-233, 1987
A;Title: Primary structure of the met protein tyrosine kinase domain.
A;Reference number: A93749; MUID:88143699; PMID:3325883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-14 <62AM>
R:Ferracini, R.; Longati, P.; Naldini, L.; Vigna, E.; Comoglio, P.M.
J. Biol. Chem. 266, 19558-19564, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1990 A;Reference number: A40175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 69; DB;
; Pred. No. 3.4;
13; Mismatches
                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: At2g18560
A;Map position: 2
C;Superfamily: flavonol O3-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.6%;
Matches 16; Conservative 1:
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EQWMN 362
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C;Accession: T13164

K;Ainberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie (Cell 95, 903-916, 1998

A;Title: Plexin A is a neuronal semaphorin receptor that controls axon guidance.
A;Reference number: 217621; MUID:99091049; PMID:9875845
A;Accession: T13164
A;Accession: T13164
A;Accession: T13164
A;Kesiques: preliminary; translated from GB/EMBL/DDBJ
A;Rosiques: 1-2051 < WINA
A;Rosiques: 1-2051 < WINA
A;Rosiques: 1-2051 < WINA
A;Gross-references: UNIPROT:096682; EMBL:AF106933; NID:94056675; PID:94056676; PIDN:AADG
C;Genetics:
A;Gene: plexB
A;Gross-references: FlyBase:PBgn0025740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: G81349
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.; Dail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVllet, A.; Whitehead, S.; Barrel C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVllet, A.; Whitehead, S.; Barrel A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA_A,Residues: 1-174 <PAR>A,Residues: 1-174 <PAR>A,Residues: 1-174 <PAR>A,Cross-references: UNIPROT: O9PPD6; GB: AL139076; GB: AL111168; NID: g6968128; PIDN: CAB7304A,Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
813.149
periplasmic nitrate reductase small chain (cytochrome C-type protein) Cj0783 [imported]
C;Species: Campylobacter jejuni
C;Species: Ampylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
C;Function:
A;Description: plays a role in neuronal cell contact, axon guidance and fasciculation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67.5; DB 2; Length 2051;
Pred. No. 19;
9; Mismatches 23; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 2; Length 174;
Pred. No. 2.5;
2; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: napB; Cj0783
C;Superfamily: cytochrome c-type protein napB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 28, 2005, 22:12:42
Job time : 7.50139 secs
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il Similarity 42.9%;
15; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.8%;
Matches 15; Conservative
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US-10-156-487A-6
US-10-474-192
US-10-474-192
US-10-474-297
US-09-912-935-23
US-10-168-365-23
US-10-168-365-34
US-09-912-935-35
US-09-912-935-35
US-09-912-935-34
US-09-912-935-34
US-09-912-935-34
US-09-912-935-34
US-09-912-935-40
US-09-912-935-40
US-09-912-935-40
US-10-052-586-472
US-10-176-758-472
US-10-176-758-772

Sequence

Sequence

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US-10-104-047-3712
                                                                                                                                                                                                      January 28, 2005, 21:59:20 ; Search time 29.518 Seconds (without alignments) 1321.880 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                       1 LSFDFPFYGHPLRQITIATG......LHHDGRIVFAYKEIPMSVPE 108
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(c) 1993 - 2005 Compugen Ltd.
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588
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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and is derived by analysis of
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seq length: 200000000
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Perfect score:
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Maximum DB
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Sequence Sequence Sequence Sequence

Sequence ' Sequence ' Sequence '

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Sequence Sequence Sequence

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64 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 123
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TITLE OF INVENTION: NO. US20030236392Alel full length cDNA
FILLE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
LENGTH: 240
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Sequence 3712, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
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US-09-912-935-36
; Sequence 36, Application US/09912935
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US-10-104-047-3712
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Sequence 230, Appl Sequence 230, Appl Sequence 2, Appli Sequence 5, Appli Sequence 179, Appl Sequence 179, Appl Sequence 192, Appl Sequence 297, Appl

US-10-104-047-3712 US-09-912-935-36 US-10-357-819-4 US-00-918-715-230 US-10-474-794-230 US-10-474-794-230 US-10-156-487A-5 US-10-156-487A-5 US-10-474-794-179 US-10-474-794-179 US-10-474-794-179 US-09-918-715-192 US-09-918-715-192

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Sequence 3712, Ap Sequence 36, Appl Sequence 36, Appl Sequence 4, Appli

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Publication No. US20040259774A1
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                         GENERAL INFORMATION
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US-09-918-715-230
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LENGTH: 488
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Childs, John
APPLICANT: Chao, Cheng-Chi
APPLICANT: Chao, Cheng-Chi
APPLICANT: Damanac, Radoje T
APPLICANT: Lee, Juhi
APPLICANT: Lee, Juhi
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 30266/37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT PILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
                    GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 588; DB 10; Best Local Similarity 100.0%; Pred. No. 2.9e-60; Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/10168365
Publication No. US20030211987A1
GENERAL INFORMATION:
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US-10-357-819-4
; Sequence 4, Application US/10357819
  US20030022825A1
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Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-168-365-36
  Publication No.
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US-10-168-365-36
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APPLICANT: ZDONG, MEAL
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-538A
CURRENT APPLICATION NUMBER: 08/10/357,819
CURRENT FILING DATE: 2000-03-08
PRIOR PLICATION NUMBER: 09/584,411
PRIOR APPLICATION NUMBER: 09/584,411
PRIOR PLILING DATE: 2000-05-31
PRIOR PLILING DATE: 2000-05-31
PRIOR PLILING DATE: 2000-05-34
PRIOR PLILING DATE: 2002-02-4
PRIOR PLILING DATE: 2002-02-8
PRIOR PLILING DATE: 2002-02-02
PRIOR PLILING DATE: 2002-02-03
PRIOR PLILING DATE: 2002-02-04
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Shimkets, Richard A.
Spytek, Kimberly A.
APPLICANT: Alvarez, Enrique
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
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Miller, Charles E.
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Rastelli, Luca
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Ji, Weizhen
Kekuda, Ramesh
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APPLICANT: Spycek, Kimberly A.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-538A
CURRENT APPLICATION NUMBER: US/10/357,819
CURRENT FILING DATE: 2003-02-03
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                                                              GARRAL INFORMATION:

APPLICANT: Carcon-Walter, Bleanor

APPLICANT: Carcon-Walter, Brad

APPLICANT: Vogelstein, Bert

APPLICANT: Wischer, Kinneth

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT FILING DATE: 2003-10-14

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR PILING DATE: 2001-04-11

PRIOR PILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359

SEQ ID NOS: 359

LENGTH: 500

LENGTH: 500
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; Pred. No. 3.5e-60;
0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/520, 781
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 09/584,411
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 10/085,198
PRIOR FILING DATE: 2002-02-14
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FILING DATE: 2002-02-01
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APPLICATION NUMBER: 60/355,099
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Publication No. US20040259774A1
GENERAL INFORMATION:
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Spytek, Kimberly A.
Zhong, Mei
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APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
Publication No. US20040213793A1
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Miller, Charles E.
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Shenoy, Suresh G.
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Best Local Similarity 100.0
Matches 108; Conservative
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Kekuda, Ramesh
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APPLICANT:
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                               TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 06/22,599
PRIOR APPLICATION NUMBER: 60/22,599
PRIOR APPLICATION NUMBER: 60/22,599
PRIOR PLILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SEQ ID NOS: 358
LENGTH: 500
LENGTH: 500
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; Pred. No. 3.5e-60;
0; Mismatches 0;
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100.0%; Pred. No. 3.5e-60;
live 0; Mismatches 0;
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US-10-474-794-230
; Sequence 230, Application US/10474794
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    Kenneth Kinzler
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Matches 108; Conservative
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US-09-918-715-230
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ORGANISM: Homo sapiens
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APPLICANT: Juan, Todd; APPLICANT: Juan, Todd; APPLICANT: Dass, Michael B.; APPLICANT: Oliner, John; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof; FILE REFERENCE: 01-072-A; CURRENT FILING DATE: 2002-09-10; PRIOR FILING DATE: 2002-09-10; PRIOR PLICATION NUMBER: 60/293,852; PRIOR PLICATION NUMBER: 60/293,852; NUMBER OF SEQ ID NOS: 15; SOFTWARE: Patentin Ver. 2.0; SOFTWARE: Patentin V
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PRIOR APPLICATION NUMBER: 60/356,424
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER: OF SEQ ID NOS: 142
SOFTWARE: Curasequist version 0.1
SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-357-819-2
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ORGANISM: Homo sapiens
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US-09-918-715-179
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US-10-156-487A-5
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137 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVVFD 196
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Sequence 179, Application US/10474794

Publication No. US20040213793A1

GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: St. Croix, Brad

APPLICANT: Kinzler, Kenneth

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REPRENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

CURRENT APPLICATION NUMBER: 60/282,850

FRIOR APPLICATION NUMBER: 60/282,850

FRIOR APPLICATION NUMBER: 60/282,850

FRIOR PILING DATE: 2001-04-11

PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Kenneth Kinzler

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILLS REPERSENCE: 1107.00134

CURRENT APPLICATION NUMBER: 06/0222, 599
FRICH APPLICATION NUMBER: 60/222, 599
FRICH APPLICATION NUMBER: 60/224, 360
FRICH APPLICATION NUMBER: 60/224, 360
FRICH APPLICATION NUMBER: 60/224, 360
FRICH APPLICATION NUMBER: 60/224, 360
FRICH APPLICATION NUMBER: 60/224, 360
FRICH APPLICATION NUMBER: 60/224, 360
FRICH APPLICATION NUMBER: 60/224, 360
FRICH FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 179
LENGTH: 1002
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100.0%; Pred. No. 8.4e-60;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 108; Conservative C
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US-10-474-794-179
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US-09-918-715-192
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Publication No. US20030017157A1

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ORGANISM: Mus musculus US-10-474-794-192
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                     RESULT 14
JS-10-156-487A-6
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Pred. No. 3.9e-53;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 500;
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Fublication No. US2003001715741
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelatein
APPLICANT: Bert Vogelatein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERRENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 00/224,599
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-04-11
SPRIOR PLING DATE: 2000-04-11
SRIOR PLING DATE: 2000-04-11
SOFTWARE: FREESQ for Windows Version 3.0
SSG ID NO 297
LENGTH: 500
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert objected:
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 192
LENGTH: 500
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Pred. No. 3.9e-53;
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91.5%;
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Best Local Similarity 91.55
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Best Local Similarity 91.5'
Matches 97; Conservative
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CORGANISM: Mus musculus
US-09-918-715-192
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US-09-918-715-297
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198 NGTVFVVQWDHVYLQDREDRGSFTFQAALHRDGRIVFGYKEIPMAV 243

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APPLICANT: Juan, Todd
APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Oliner: John
TITLE OF INVENITON: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT PEPLICATION NUMBER: US/10/156,487A
CURRENT FILING DATE: 2002-09-10
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Pred. No. 3.9e-53;
4; Mismatches 5; Indels (
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; Sequence 192, Application US/10474794
; Publication No. USZO040213793A1
; GENERAL INFORMATION:
    APPLICANT: Carson-Walter, Eleanor
    APPLICANT: Carson-Walter, Eleanor
    APPLICANT: Wog-latein, Bart
    APPLICANT: Wog-latein, Bart
    APPLICANT: Kinzler, Kenneth
    TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
    TITLE REFERENCE: 1107.00179
    CURRENT APPLICATION: NUMBER: US/10/44,794
    CURRENT APPLICATION NUMBER: 60/282,850
    PRIOR APPLICATION NUMBER: 60/308,829
    PRIOR FILING DATE: 2001-08-01
    NUMBER OF SEQ ID NOSE: 359
    SOFTWARE: FastSEQ for Windows Version 4.0
    TENNOW: 1000
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Sequence 6, Application US/10156487A Publication No. US20030092025A1 GENERAL INFORMATION:
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Best Local Similarity 91.5%;
Matches 97; Conservative
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Best Local Similarity 91.51
Matches 97; Conservative
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Sequence 25, Appl
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Sequence 1995, Appli
Sequence 1995, Appli
Sequence 16, Appli
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Sequence 16, Appli
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Sequence 4675, Appli
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Sequence 4, Appli
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816.164 Million cell updates/sec
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                                                                                      January 28, 2005, 21:56:43 ; Search time 8.77562 Seconds
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. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-09-764-325A-23
US-09-764-325A-25
US-09-912-935-23
US-09-912-935-35
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US-09-912-935-35
US-09-912-935-36
US-09-912-935-38
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US-09-912-935-38
US-09-912-935-38
US-08-746-797-2
US-08-912-935-38
US-08-746-797-2
US-08-746-797-2
US-08-746-797-2
US-08-746-797-2
US-08-918-088-2
US-08-918-088-3
US-09-543-681A-4675
US-09-543-681A-4675
US-09-634-856A-4
US-09-635-705-4
US-09-635-705-4
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US-09-270-767-46295
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588
             GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTION VERSION 3.0
SEQ ID NO 36
LENGTH 431
TYPE: PRT
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US-09-764-325A-23

Sequence 23, Application US/09764325A

Fatent No. 6667391

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Chao, Cheng-Chi
APPLICANT: Childs, John
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
FILE REFERENCE: 30266/37630A

CURRENT APPLICATION NUMBER: US/09/764,325A

CURRENT FILING DAIE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2877, Ap
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                                                    US-09-195-666A-49
US-09-309-502-6
US-09-303-502-6
US-09-635-705-49
US-09-634-858A-5
US-09-634-858A-5
US-09-634-858A-9
US-09-927C-49
US-09-927C-49
US-09-257-555A-9
US-09-211-540-6
US-09-342-394-2
US-09-342-394-2
US-09-118-709-2
US-09-718-709-2
US-09-718-709-2
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Best Local Similarity 100.
Matches 108; Conservative
                                                          ORGANISM: Homo sapiens
US-09-912-935-36
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| JAPPLICANT: Labat, Ivan
| APPLICANT: Labat, Ivan
| APPLICANT: Tang, Y. T. T. APPLICANT: Tang, Y. T. T. APPLICANT: Tang, Y. T. T. APPLICANT: Tang, Cheng-Chi
| APPLICANT: Tang, Cheng-Chi
| APPLICANT: Chao, Cheng-Chi
| APPLICANT: Childs, John
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
| TITLE OF INVENTION WHERE: USO/9/64,325A
| TITLE OF INVENTION NUMBER: USO/9/44,325A
| CURRENT APPLICATION NUMBER: 09/547,358
| PRIOR APPLICATION NUMBER: 09/545,714
| PRIOR PILING DATE: 2000-04-07
| PRIOR PILING DATE: 2000-04-07
| PRIOR PILING DATE: 2000-04-07
| PRIOR PILING DATE: 2000-01-21
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 25
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PRIOR APPLICATION NUMBER: US/54/,530
PRIOR FILING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 392
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; Sequence 23, Application US/09912935
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM:
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Sequence 25, Application US/09912935

Sequence 25, Application US/09912935

Sequence 25, Application US/09912935

Patent No. 6673904

GRNERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2000-12-23

NUMBER: OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 25

LENGTH: 392
GREERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 32066/37483
CURRENT PAPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 392
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APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Indels
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Best Local Similarity 72.2%
Matches 78; Conservative
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US-09-912-935-25
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US-09-912-935-23
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Best Local Similarity
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US-09-912-935-35
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Sequence 40, Application US/09912935
Sequence 40, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPRENCE: 32066/3748
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTING OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTING OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: 2066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
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                                                                                                                                                                                                                                                           18; Indels
                                                                                                                                                                                                     70.9%; Score 417; DB 4; 72.2%; Pred. No. 1.5e-44; rative 12; Mismatches 18;
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Patent No. 6673904
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 3.1
LENGTH: 499
                                                                                                                                                                                                                                                              78; Conservative
                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-912-935-28
                                                                                                                                                                                                        Query Match
Best Local Similarity
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LENGTH: 529
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                                                                                                                                                                                                                                                           Matches
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APPLICANT: Nishikawa, Mitsuo et al.

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2001-07-24

PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.0

SEQ ID NO 34
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Sequence 31, Application US/09912935

Patent No. 6673904

GENERAL INFORMATION: Mitsuo et al.

APPLICAUT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2010-10-24

PRIOR FILING DATE: 2000-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.9%; Score 417; DB 4; Length 449; Best Local Similarity 72.2%; Pred. No. 1.3e-44; Matches 78; Conservative 12; Mismatches 18; Indels
                CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
LENGTH: 425
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     FILE REFERENCE: 32066/37483
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-912-935-34
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                                                                                            CLASSIFICATION:
PRIOR APPLICATION
APPLICATION UNUBER: No. 5759832 Yet Assigned
FILING DATE: 23-OCT-1996
ATTORNEY/ABENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
TELECOMMIXICATION INFORMATION:
TELECOMMIXICATION INFORMATION:
TELECOMMIXICATION INFORMATION:
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Patent No. 5783422
GENERAL INFORMATION:
APPLICANT: Centry, Daniel
APPLICANT: Lonsdale, John
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.6%; Score 68; DB 3
Best Local Similarity 23.5%; Pred. No. 2.6;
Matches 31; Conservative 19; Mismatches
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COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
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220 FAIRDVAKSIKQ 231
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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US-08-927-387-2
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Sequence 38, Application US/09912935
Sequence 38, Application US/09912935
Sequence 38, Application US/09912935
Sequence 38, Application US/0904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 38
LENGTH: 530
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                                                                                                                                                                                                                                                                                 1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
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                                                                                                      Length 529;
                                                                                                                                                                      18; Indels
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GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Parseon, Stewart
TITLE OF INVENTION: NOVEL FabH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SmithKine Beecham Corporation
STREET: 709 Swedeland Road
CITY: Ring of Prussia
                                                                                               70.9%; Score 417; DB 4; 72.2%; Pred. No. 1.6e-44; iive 12; Mismatches 18;
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                                                      Query Match
Best Local Similarity 72.2$
-دءه 78; Conservative
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Matches 76; Conservative
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
; ORGANISM: Homo sapiens
US-09-912-935-40
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ORGANISM: Mouse
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46; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 ITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPG
                                                                                                                                                                                                                                                                                                                                                                                                          11.6%; Score 68; DB 1
23.5%; Pred. No. 2.6;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GTVFVV----QWDHVYLQGWEDKGS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,058
FILING DATE: 25-AUG-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/746,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
APPLICANT: Lonadale, John
APPLICANT: Payne, David
APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FabH
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham (
APPLICATION NUMBER: 08/746,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-918-058-2; Application US/08918058; Patent No. 5885572
           FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward:
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P505'
TELECOMUNICATION INFORMATION:
TELECHONE: 610-270-4478
TELEPAN: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.5'
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || ::: |: :
220 FAIRDVAKSIKQ 231
                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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Sequence 7887, Application US/09543681A

Factor 7887, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 2709, 1002-01

CURRENT APPLICATION WUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 GAGGVILEASEQEHFLAESINSDGSRSECLTYGHSGLHSPFSDQESADSFLKMDGRTVFD 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TIATGGFIFMGDVIHRMLTATQYVAPL--MANFNPGYSDNSTVVYFDNGTVFVVQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 ITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPG-
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11.6%; Score 68; DB 2
Best Local Similarity 23.5%; Pred. No. 2.6;
Matches 31; Conservative 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 ---WDH-----VYLQGWEDKGS 82
REFERENCE/DOCKET NUMBER: P5
FELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                           TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
ENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7887
                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.5*
Matches 22; Conservative
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220 FAIRDVAKSIKQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 FAYKEIPMSVPE 108
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N

ORIGINAL SOURCE:
US-08-918-058-2
                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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996e59 homo sapien

996e59 homo sapien

996d9 homo sapien

Aaq88850 homo sapien

Aaq88850 homo sapien

906e55 wenopus lae

060e17 mus musculu

0912v6 mus musculu

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Adq62573 xenopus 1
P79691 carassius a
P79838 puntius con
P79850 puntius tet
P79858 rasbora ele
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Q91zv7 mus musculu
Q8bm20 mus musculu
Q66e59 homo sapien
Q6ux71 homo sapien
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Q8iuk5 homo sapien
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                                                                                                                 ; Search time 36.7978 Seconds (without alignments)
1688.701 Million cell updates/sec
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                                                                                                                                                                                          US-09-918-715-230_COPY_137_244
588
1 LSPDFPFYGHPLRQITIATG........LHHDGRIVFAYKEIPMSVPE 108
                                                                                                                                                                                                                                                                                                                                                                           1825181
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                 January 28, 2005, 21:55:21; Search
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
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OGURRB
AAQ62573
SHH_CARAU
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SHH_RASEL
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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1161
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Match
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Maximum DB
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anopheles g
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danio aequi
danio frank
danio frank
danio kerri
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                        tanichthys
gallus gall
drosophila
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                                                                                                     drosophila
drosophila
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EMBL, AK127539; BAC87025.1; --
EMBL, AK127539; Plaxin_repeat.

R Interpro; IPRO02165; Plaxin_repeat.

R Pfam; PFO1437; PSI; 1.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
towner endothelial marker 7 (TEM7).
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein FLJ45632.

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        P79915 t
Q9yh85 g
Q9yh85 g
Q8mmc7 q
Q9wmc7 q
Q7q440 s
Q7q440 s
Q13235 q
Q13234 q
Q13238 q
Q13238 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AA
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                     SHH_TANAL
TECA_CHICK
Q7JN86
Q9JN078
SHH AMBCH
Q7Q440
SHH DANAA
SHH_DANAA
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SHH DANFR
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SHH DANPU
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Best Local Similarity 100.0
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                   Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamasu A., Umezawa A., Imabayashi H., Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nasmura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyam S., Nagahari K., Masuho Y., Nagai K., Isogai T., "NEDO human cDNA sequencing project.";
"NEDO human CDNA sequencing project.";
submitted (JUL-203) to the EMBL/GenBank/DDBJ databases.
EMBL, AK127539; BAC87025.1; -
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MEDLINE=21443268; PubMed=11559528;
MEDLINE=2144326B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-ORT-2001 (TrEMBLrel. 18, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor endothelial marker 7 precursor (Tumor endothelial marker 3
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Vogelstein B.,
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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St Croix B., Rago C., Velculescu V., Traverso G.,
Montgomery E., Lal A., Riggins G.J., Lengauer C.,
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; Pred. No. 6.8e-54;
0; Mismatches 0;
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Widin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKeman D.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

R. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Halton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Richards M., Saliska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

and mouse S.J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036659; AAH36659.1;
Genew; HGNC:20945; PLXDC1.
GO, GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
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E 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIKEN FANTOM Consortium; "Punctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                01-JUN-2001 (TYEMBLrel. 17, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
Name=Plxdc1,
                                             61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                                   Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
MEDLINE=21085660; PubMed=11217851;
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MEDLINE=99279253; PubMed=10349636;
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                                                                                                                                                                                                               PRELIMINARY;
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Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C.,
Sakai K.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.; Yasunishi A., Yoshida K., Yoshino M.,
Embi, AKO1051; BAB26881.1; -.
GO, GO:0016229; E:receptor activity; IEA.
GO, GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LSPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
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91.5%; Pred. No. 2.4e-47;
ive 4; Mismatches 5; Indels
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MEDLINE-21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
tumor endothelial marker 7.
14FE25512A319DAF CRC64;
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InterPro; IPR003659; Plexin-like.
InterPro; IPR013659; Plexin-like.
InterPro; IPR01365; Plexin-repeat.
Fam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
Tumor endothelial marker 7 precursor.
Name=Plxdc1, Synonyme=Tem7;
Mus musculus (Mouse)
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RMBL, AF978760; AAL11997.1; --

MGD; MGI.1919574; Plxdc1.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007575; F:redevelopment; IEA.

InterPro; IPR007110; IG-11ke.

InterPro; IPR003659; Plexin-like.
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nes 97; Conservative
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PLXDC2 protein.
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                      SEQUENCE FROM N.A.

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SEQUENCE TISSUB-Cerebellum;

SEQUENCE TISSUB-Cerebellum;

A Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Takiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771 (2000).
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SYRALM=CS7BL/G4J TISSUB=Cerebellum;
MEDLINE=C37BL/G409374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wornalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate cerebellum CDNA, RIKEN full-length
enriched library, clone:96300400L07 product:TUMOR ENDOTHELIAL MARKER
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STRAIN=CS7BL/6J; TISSUE=Cerebellum;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=C57BL/6J; TISSUE-Cerebellum;
MEDLINE=2108566); PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                           NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
                                                                                                                    198 NGTVFVVQWDHVYLQDREDRGSFTFQAALHRDGRIVFGYKEIPMAV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Yi.
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                             Created)
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STRAIN=C57BL/6J; IISSUE=Cerebellum;
The FANTOM Consortium,
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Controlling F.S., Wagner L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Brothero M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Potens G.J., Abramson R.D., Mullahy S.J.,
A Brosak S.S., McZwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
A Brosak S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pakey J., Helton B.K. Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
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Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nakamira M., Nakamira M., Nakamira M., Nakamira M., Saitoh H., Saitoh H., Sakai C., Sakai K., Sakazume N., Okazaki Y., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawi T., Tagawa A., Takahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Embl., AKO36144; BAC2918.1; -
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00423; PSI; 1.
SROUTENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;
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Last annotation update)
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 528; DB 2; L 91.5%; Pred. No. 2.4e-47; tive 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 AA.
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007275; P:development; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.5%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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221 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
529
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12975309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                humans."
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                                                                    Q96PD9
                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
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                                            RESULT 10
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                                                                                                                                                                                                                                           1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLFATQYVAPLMANFNPGYSDNSTVVYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jinn Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                             172 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.9%; Score 417; DB 2; Length 529; 72.2%; Pred. No. 1.5e-35; ive 12; Mismatches 18; Indel8
                                                                                                                                                                                        Length 480;
                                                                                                                                                                                      70.9%; Score 417; DB 2; Length 48 72.2%; Pred. No. 1.3e-35; ive 12; Mismatches 18; Indels
SEQUENCE FROM N.A.

TISSUB=Ovary;
Strauberg R.;
Submitted (40G-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012885; AAH12885.1; -.
EMBL; BC012885; Camenbrane; IEA.
GO; GO:0006472; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
                                                                                                          529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         529 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bioinformatics assessment.";
Genome Res. 13.256.2270(2003).
EMBL; A758446; AAQ88850.1; ...
Interpro; IPR003659; Plexin-like.
Interpro; IPR002165; Plexin_repeat.
Pfam; PP01437; PS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22887296; PubMed=12975309;
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                     Local Similarity
tes 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=UNQ2514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                        Query Match
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Q6UX71
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1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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                                                                                                                                                                                                                                                                           MEDLINE=21443268; PubMed=11559528;
Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor endothelial marker 7-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.9%; Score 417; DB 2; Length 529;
72.2%; Pred. No. 1.5e-35;
tive 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 529 tumor endothellal marker , 529 AA; 59583 MW; D44A0975DF894840 CRC64;
                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Tumor endothelial marker 7-related precursor.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew, HGNC:21013; PLXDC2.
Go; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR0031659; Plexin_like.
InterPro; IPR002165; Plexin_repeat.
Fan; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                          Cancer Res. 61:6649-6655(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF378757; AAL11994.1; -.
01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 72.2%
les 78; Conservative
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                       Query Match
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B scheetz T.E.,
K Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
K Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
And Bronse S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                    ô
                                                                                                                                                                                                            1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
                                         "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
                                                                                                                                                                    Gaps
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
BEDLINE-22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                  61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                                                                                                         Length 529;
                                                                                                                                                                  18; Indels
                                                                    Bioinformatics Assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AY358486; AAQ88850.1; -
SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2004 (TrEMBLrel. 28, Last sequence update) 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                       70.9%; Score 417; DB 2; 72.2%; Pred. No. 1.5e-35; ive 12; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                  513 AA
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                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
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                                                                                                                                                   Local Similarity
tes 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
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                                                                                                                                         Query Match
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STRAIN-MRK; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

X STRAIN-MRK; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

X Straubberg R.L., Feligold E.A., Grous L.H., Derge J.G.,

X Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phytins R.F., Jordan H., Noore T., Max S.I., Wang J., Hshelf F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nordriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"The strand of the sequences.";
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                                                                                                                                                                                                                                                                                                1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=NVRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.9%; Score 411; DB 2; Length 530; ilarity 70.4%; Pred. No. 6.4e-35; Conservative 13; Mismatches 19; Indels
                                                                                                                                                   Length 513;
                                                                                                                                                   70.2%; Score 413; DB 2; Length 51 72.6%; Pred. No. 3.8e-35; tive 12; Mismatches 17; Indels
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EMBL; BC077242; AAH77242.1; -.
Hypothetical protein.
SEQUENCE 513 Aa; 57622 MW; 301EA53F2905A4ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00423; PSI; 1.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequ
05-JUL-2004 (TrEMBLrel. 27, Last anno
05-JUL-2004 (TrEMBLrel. 27, Last anno
05-JUL-2004 (TrEMBLrel. 27, Last anno
05-JUL-2004 (TrEMBLrel. 7-related,
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Matches 77; Conservative
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Best Local Similarity
Matches 76; Conserv
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SEQUENCE
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161 LSFDFPFYGHFLNEVTVATGGFIYTGEVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFD 220
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C STRAIN=C57BL/6J; TISSUB=Lung;

X MEDLINE=205:0913; Pubmed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Kiteunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

A Pujiwake S., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUB=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
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STRAIN-CSTBL/60; TISSUE-Lung;
Adachi J., Alzawa T., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=21085660; PubMed=11217851;
MIKEN FANTOM CONSOrtium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                     NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
Carpinci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN-C57BL/6J; TISSUE-Lung;
The FANTOM CONSOITIUM,
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Q9DC11
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RA Emotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Rawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohino M.,
RA Okazaki Y., Okido T., Owato T., Saito H., Salto R., Sakai C.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Jejima Y., Toya T., Yamamura T., Yasunishi P., Tanaka T.,
R Tejima Y., Toya T., Yamamura T., Yasunishi R., Yoshino M.,
R Muramatsu M., Hayashizaki Y.;
Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.
R MDP, MII:1914698; Plxdc2.
BR GO; GO:0016020; C:membrane; IEA.
BR GO; GO:0004872; F:receptor activity; IEA.
BR GO; GO:000482; F:receptor activity; IEA.
BR InterPro; IPR00359; Plexin-like.
R InterPro; IPR00359; Plexin-like.
R InterPro; IPR00155; Plexin-like.
R InterPro; PR00155; Plexin-like.
R INTERPRO; RP001515; Plexin-like.
R SMART; SM00423; PSI; 1.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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tumor endothelial marker 7-related.
FF8315020735E36D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.9%; Score 411; DB 2; Length 530; ilarity 70.4%; Pred. No. 6.4e-35; Conservative 13; Mismatches 19; Indels
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EMBL; AF378761; AAL11998.1; -.
MGD; MGI:1914698; Plxdc2.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000755; P:redevelopment; IEA.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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Mus musculus (Mouse).
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SMART; SM00423; PSI; 1.
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530 AA;
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Best Local Similarity
Matches 76; Conserv
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        QY
        1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNFGYSDNSTVVYFD 60

        DD
        161 LSFDFPFYGHFLNEVYTATGGFIYTGEVVHRMLTATQYYAPLMANFDFSVSRNSTVRYFD 220

        QY
        61 NGTVFVVQWDHVYLQQMEDKGSFFTFQALLHHDGRIVFAYKEIPMSVPE 108

        C
        1 NGTVFVVQWDHVYLQQDNYNLGSFTFQALLHHDGRIVFAYKEIPWLYQ 268

        DD
        221 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVYQ 268
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